



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C07K 14/47, 14/82, 14/15, C12Q 1/68, G01N 33/574, A61K 38/17, 39/00		A2	(11) International Publication Number: WO 98/45328 (43) International Publication Date: 15 October 1998 (15.10.98)
(21) International Application Number: PCT/US98/06939 (22) International Filing Date: 9 April 1998 (09.04.98)	(81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).		
(30) Priority Data: 08/838,762 9 April 1997 (09.04.97) US 08/991,789 11 December 1997 (11.12.97) US			
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(54) Title: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER

(57) Abstract

Compositions and methods for the detection and therapy of breast cancer are disclosed. The compounds provided include nucleotide sequences that are preferentially expressed in breast tumor tissue, as well as polypeptides encoded by such nucleotide sequences. Vaccines and pharmaceutical compositions comprising such compounds are also provided and may be used, for example, for the prevention and treatment of breast cancer. The polypeptides may also be used for the production of antibodies, which are useful for diagnosing and monitoring the progression of breast cancer patient.

Published

Without international search report and to be republished upon receipt of that report.

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COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER

TECHNICAL FIELD

The present invention relates generally to the detection and therapy of 5 breast cancer. The invention is more specifically related to nucleotide sequences that are preferentially expressed in breast tumor tissue and to polypeptides encoded by such nucleotide sequences. The nucleotide sequences and polypeptides may be used in vaccines and pharmaceutical compositions for the prevention and treatment of breast cancer. The polypeptides may also be used for the production of compounds, such as 10 antibodies, useful for diagnosing and monitoring the progression of breast cancer in a patient.

BACKGROUND OF THE INVENTION

Breast cancer is a significant health problem for women in the United States and throughout the world. Although advances have been made in detection and 15 treatment of the disease, breast cancer remains the second leading cause of cancer-related deaths in women, affecting more than 180,000 women in the United States each year. For women in North America, the life-time odds of getting breast cancer are now one in eight.

No vaccine or other universally successful method for the prevention or 20 treatment of breast cancer is currently available. Management of the disease currently relies on a combination of early diagnosis (through routine breast screening procedures) and aggressive treatment, which may include one or more of a variety of treatments such as surgery, radiotherapy, chemotherapy and hormone therapy. The course of treatment for a particular breast cancer is often selected based on a variety of prognostic 25 parameters, including an analysis of specific tumor markers. *See, e.g.,* Porter-Jordan and Lippman, *Breast Cancer* 8:73-100 (1994). However, the use of established markers often leads to a result that is difficult to interpret, and the high mortality observed in

breast cancer patients indicates that improvements are needed in the treatment, diagnosis and prevention of the disease.

Accordingly, there is a need in the art for improved methods for therapy and diagnosis of breast cancer. The present invention fulfills these needs and further 5 provides other related advantages.

SUMMARY OF THE INVENTION

Briefly stated, the subject invention provides compositions and methods for the diagnosis and therapy of breast cancer. In one aspect, isolated DNA molecules are provided, comprising (a) a nucleotide sequence preferentially expressed in breast 10 cancer tissue, relative to normal tissue; (b) a variant of such a sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% (preferably no more than 5%) of the nucleotide positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained; or (c) a nucleotide sequence encoding an epitope of a polypeptide 15 encoded by at least one of the above sequences. In one embodiment, the isolated DNA molecule comprises a human endogenous retroviral sequence recited in SEQ ID NO:1. In other embodiments, the isolated DNA molecule comprises a nucleotide sequence recited in any one of SEQ ID NO: 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 20 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.

In related embodiments, the isolated DNA molecule encodes an epitope of a polypeptide, wherein the polypeptide is encoded by a nucleotide sequence that: (a) hybridizes to a sequence recited in any one of SEQ ID NO: 1, 3-26, 28-77, 142, 143, 25 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297 under stringent conditions; and (b) is at least 80% identical to a sequence recited in any one of SEQ ID NO: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219,

221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297; and wherein RNA corresponding to said nucleotide sequence is expressed at a greater level in human breast tumor tissue than in normal breast tissue.

5 In another embodiment, the present invention provides an isolated DNA molecule encoding an epitope of a polypeptide, the polypeptide being encoded by: (a) a nucleotide sequence transcribed from the sequence of SEQ ID NO: 141; or (b) a variant of said nucleotide sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide 10 positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained. Isolated DNA and RNA molecules comprising a nucleotide sequence complementary to a DNA molecule as described above are also provided.

15 In related aspects, the present invention provides recombinant expression vectors comprising a DNA molecule as described above and host cells transformed or transfected with such expression vectors.

 In further aspects, polypeptides, comprising an amino acid sequence encoded by a DNA molecule as described above, and monoclonal antibodies that bind to such polypeptides are provided.

20 In yet another aspect, methods are provided for determining the presence of breast cancer in a patient. In one embodiment, the method comprises detecting, within a biological sample, a polypeptide as described above. In another embodiment, the method comprises detecting, within a biological sample, an RNA molecule encoding a polypeptide as described above. In yet another embodiment, the method 25 comprises (a) intradermally injecting a patient with a polypeptide as described above; and (b) detecting an immune response on the patient's skin and therefrom detecting the presence of breast cancer in the patient. In further embodiments, the present invention provides methods for determining the presence of breast cancer in a patient as described above wherein the polypeptide is encoded by a nucleotide sequence selected from the 30 group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208,

215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

In a related aspect, diagnostic kits useful in the determination of breast cancer are provided. The diagnostic kits generally comprise either one or more 5 monoclonal antibodies as described above, or one or more monoclonal antibodies that bind to a polypeptide encoded by a nucleotide sequence selected from the group consisting of sequences provided in SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 and 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and a detection reagent.

10 Within a related aspect, the diagnostic kit comprises a first polymerase chain reaction primer and a second polymerase chain reaction primer, at least one of the primers being specific for an RNA molecule described herein. In one embodiment, at least one of the primers comprises at least about 10 contiguous nucleotides of an RNA molecule as described above, or an RNA molecule encoding a polypeptide encoded by a 15 nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

Within another related aspect, the diagnostic kit comprises at least one oligonucleotide probe, the probe being specific for a DNA molecule described herein. 20 In one embodiment, the probe comprises at least about 15 contiguous nucleotides of a DNA molecule as described above, or a DNA molecule selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

25 In another related aspect, the present invention provides methods for monitoring the progression of breast cancer in a patient. In one embodiment, the method comprises: (a) detecting an amount, in a biological sample, of a polypeptide as described above at a first point in time; (b) repeating step (a) at a subsequent point in time; and (c) comparing the amounts of polypeptide detected in steps (a) and (b), and 30 therefrom monitoring the progression of breast cancer in the patient. In another

embodiment, the method comprises (a) detecting an amount, within a biological sample, of an RNA molecule encoding a polypeptide as described above at a first point in time; (b) repeating step (a) at a subsequent point in time; and (c) comparing the amounts of RNA molecules detected in steps (a) and (b), and therefrom monitoring the progression 5 of breast cancer in the patient. In yet other embodiments, the present invention provides methods for monitoring the progression of breast cancer in a patient as described above wherein the polypeptide is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285- 10 287, 289, 290 and sequences that hybridize thereto under stringent conditions.

In still other aspects, pharmaceutical compositions, which comprise a polypeptide as described above in combination with a physiologically acceptable carrier, and vaccines, which comprise a polypeptide as described above in combination with an immune response enhancer or adjuvant, are provided. In yet other aspects, the 15 present invention provides pharmaceutical compositions and vaccines comprising a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 and 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

20 In related aspects, the present invention provides methods for inhibiting the development of breast cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as described above.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All 25 references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the differential display PCR products, separated by gel electrophoresis, obtained from cDNA prepared from normal breast tissue (lanes 1 and 2)

and from cDNA prepared from breast tumor tissue from the same patient (lanes 3 and 4). The arrow indicates the band corresponding to B18Ag1.

Figure 2 is a northern blot comparing the level of B18Ag1 mRNA in breast tumor tissue (lane 1) with the level in normal breast tissue.

5 Figure 3 shows the level of B18Ag1 mRNA in breast tumor tissue compared to that in various normal and non-breast tumor tissues as determined by RNase protection assays.

Figure 4 is a genomic clone map showing the location of additional retroviral sequences obtained from ends of XbaI restriction digests (provided in SEQ ID
10 NO:3 - SEQ ID NO:10) relative to B18Ag1.

Figures 5A and 5B show the sequencing strategy, genomic organization and predicted open reading frame for the retroviral element containing B18Ag1.

Figure 6 shows the nucleotide sequence of the representative breast tumor-specific cDNA B18Ag1.

15 Figure 7 shows the nucleotide sequence of the representative breast tumor-specific cDNA B17Ag1.

Figure 8 shows the nucleotide sequence of the representative breast tumor-specific cDNA B17Ag2.

20 Figure 9 shows the nucleotide sequence of the representative breast tumor-specific cDNA B13Ag2a.

Figure 10 shows the nucleotide sequence of the representative breast tumor-specific cDNA B13Ag1b.

Figure 11 shows the nucleotide sequence of the representative breast tumor-specific cDNA B13Ag1a.

25 Figure 12 shows the nucleotide sequence of the representative breast tumor-specific cDNA B11Ag1.

Figure 13 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA3c.

30 Figure 14 shows the nucleotide sequence of the representative breast tumor-specific cDNA B9CG1.

Figure 15 shows the nucleotide sequence of the representative breast tumor-specific cDNA B9CG3.

Figure 16 shows the nucleotide sequence of the representative breast tumor-specific cDNA B2CA2.

5 Figure 17 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA1.

Figure 18 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA2.

10 Figure 19 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA3.

Figure 20 shows the nucleotide sequence of the representative breast tumor-specific cDNA B4CA1.

Figure 21A depicts RT-PCR analysis of breast tumor genes in breast tumor tissues (lanes 1-8) and normal breast tissues (lanes 9-13) and H₂O (lane 14).

15 Figure 21B depicts RT-PCR analysis of breast tumor genes in prostate tumors (lane 1, 2), colon tumors (lane 3), lung tumor (lane 4), normal prostate (lane 5), normal colon (lane 6), normal kidney (lane 7), normal liver (lane 8), normal lung (lane 9), normal ovary (lanes 10, 18), normal pancreases (lanes 11, 12), normal skeletal muscle (lane 13), normal skin (lane 14), normal stomach (lane 15), normal testes (lane 20) 16), normal small intestine (lane 17), HBL-100 (lane 19), MCF-12A (lane 20), breast tumors (lanes 21-23), H₂O (lane 24), and colon tumor (lane 25).

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the diagnosis, monitoring and therapy of breast cancer.

25 The compositions described herein include polypeptides, nucleic acid sequences and antibodies. Polypeptides of the present invention generally comprise at least a portion of a protein that is expressed at a greater level in human breast tumor tissue than in normal breast tissue (*i.e.*, the level of RNA encoding the polypeptide is at least 2-fold higher in tumor tissue). Such polypeptides are referred to herein as breast tumor-

specific polypeptides, and cDNA molecules encoding such polypeptides are referred to as breast tumor-specific cDNAs. Nucleic acid sequences of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of a polypeptide as described above, or that is complementary to such a sequence.

5 Antibodies are generally immune system proteins, or fragments thereof, that are capable of binding to a portion of a polypeptide as described above. Antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies.

10 Polypeptides within the scope of this invention include, but are not limited to, polypeptides (and epitopes thereof) encoded by a human endogenous retroviral sequence, such as the sequence designated B18Ag1 (Figure 5 and SEQ ID NO:1). Also within the scope of the present invention are polypeptides encoded by other sequences within the retroviral genome containing B18Ag1 (SEQ ID NO: 141).

15 Such sequences include, but are not limited to, the sequences recited in SEQ ID NO:3 - SEQ ID NO:10. B18Ag1 has homology to the *gag* p30 gene of the endogenous human retroviral element S71, as described in Werner et al., *Virology* 174:225-238 (1990) and also shows homology to about thirty other retroviral *gag* genes. As discussed in more detail below, the present invention also includes a number of additional breast tumor-

20 specific polypeptides, such as those encoded by the nucleotide sequences recited in SEQ ID NO: 11-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including

25 full length proteins containing the sequences recited herein. A polypeptide comprising an epitope of a protein containing a sequence as described herein may consist entirely of the epitope, or may contain additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may (but need not) possess immunogenic or antigenic properties.

An "epitope," as used herein is a portion of a polypeptide that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Epitopes may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides derived from the native polypeptide for the ability to react with antigen-specific antisera and/or T-cell lines or clones. An epitope of a polypeptide is a portion that reacts with such antisera and/or T-cells at a level that is similar to the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. B-cell and T-cell epitopes may also be predicted via computer analysis. Polypeptides comprising an epitope of a polypeptide that is preferentially expressed in a tumor tissue (with or without additional amino acid sequence) are within the scope of the present invention.

The compositions and methods of the present invention also encompass variants of the above polypeptides and nucleic acid sequences encoding such polypeptides. A polypeptide "variant," as used herein, is a polypeptide that differs from the native polypeptide in substitutions and/or modifications, such that the antigenic and/or immunogenic properties of the polypeptide are retained. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antisera and/or T-cells as described above. Nucleic acid variants may contain one or more substitutions, deletions, insertions and/or modifications such that the antigenic and/or immunogenic properties of the encoded polypeptide are retained. One preferred variant of the polypeptides described herein is a variant that contains nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another

amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; 5 (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

10 Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenic or antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a 15 polypeptide may be conjugated to an immunoglobulin Fc region.

15 In general, nucleotide sequences encoding all or a portion of the polypeptides described herein may be prepared using any of several techniques. For example, cDNA molecules encoding such polypeptides may be cloned on the basis of the breast tumor-specific expression of the corresponding mRNAs, using differential display PCR. This technique compares the amplified products from RNA template prepared from normal and breast tumor tissue. cDNA may be prepared by reverse transcription of RNA using a (dT)₁₂AG primer. Following amplification of the cDNA using a random primer, a band corresponding to an amplified product specific to the tumor RNA may be cut out from a silver stained gel and subcloned into a suitable 20 vector (e.g., the T-vector, Novagen, Madison, WI). Nucleotide sequences encoding all or a portion of the breast tumor-specific polypeptides disclosed herein may be amplified from cDNA prepared as described above using the random primers shown in SEQ ID 25 NO.:87-125.

30 Alternatively, a gene encoding a polypeptide as described herein (or a portion thereof) may be amplified from human genomic DNA, or from breast tumor

cDNA, via polymerase chain reaction. For this approach, B18Ag1 sequence-specific primers may be designed based on the sequence provided in SEQ ID NO:1, and may be purchased or synthesized. One suitable primer pair for amplification from breast tumor cDNA is (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO.:126) and 5 (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO.:127). An amplified portion of B18Ag1 may then be used to isolate the full length gene from a human genomic DNA library or from a breast tumor cDNA library, using well known techniques, such as those described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY (1989). Other sequences within 10 the retroviral genome of which B18Ag1 is a part may be similarly prepared by screening human genomic libraries using B18Ag1-specific sequences as probes. Nucleotides translated into protein from the retroviral genome shown in SEQ ID NO: 141 may then be determined by cloning the corresponding cDNAs, predicting the open reading frames and cloning the appropriate cDNAs into a vector containing a viral 15 promoter, such as T7. The resulting constructs can be employed in a translation reaction, using techniques known to those of skill in the art, to identify nucleotide sequences which result in expressed protein. Similarly, primers specific for the remaining breast tumor-specific polypeptides described herein may be designed based on the nucleotide sequences provided in SEQ ID NO:11 - SEQ ID NO:86 and SEQ ID 20 NO:142 - SEQ ID NO:297.

Recombinant polypeptides encoded by the DNA sequences described above may be readily prepared from the DNA sequences. For example, supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. 25 Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

In general, any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this 30 invention. Expression may be achieved in any appropriate host cell that has been

transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO.

5 Such techniques may also be used to prepare polypeptides comprising epitopes or variants of the native polypeptides. For example, variants of a native polypeptide may generally be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis, and sections of the DNA sequence may be removed to permit preparation of truncated polypeptides. Portions and other
10 variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing
15 amino acid chain. *See Merrifield, J. Am. Chem. Soc.* 85:2149-2146 (1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division, Foster City, CA, and may be operated according to the manufacturer's instructions.

20 In specific embodiments, polypeptides of the present invention encompass amino acid sequences encoded by a DNA molecule having a sequence recited in any one of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297, variants of such polypeptides that are encoded by DNA molecules containing
25 one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions, and epitopes of the above polypeptides. Polypeptides within the scope of the present invention also include polypeptides (and epitopes thereof) encoded by DNA sequences that hybridize to a DNA molecule having a sequence recited in any one of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-
30 166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240,

243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297 under stringent conditions, wherein the DNA sequences are at least 80% identical in overall sequence to a recited sequence and wherein RNA corresponding to the nucleotide sequence is expressed at a greater level in human breast
5 tumor tissue than in normal breast tissue. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65°C and two washes of 30 minutes each in 0.2 X SSC, 0.1% SDS at 65°C. DNA molecules according to the present invention include molecules that encode any of the
10 above polypeptides.

In another aspect of the present invention, antibodies are provided. Such antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen
15 comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole
20 limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

25 Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519 (1976), and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may
30 be produced, for example, from spleen cells obtained from an animal immunized as

described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and 5 then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having 10 high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from 15 the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Antibodies may be used, for example, in methods for detecting breast 20 cancer in a patient. Such methods involve using an antibody to detect the presence or absence of a breast tumor-specific polypeptide as described herein in a suitable biological sample. As used herein, suitable biological samples include tumor or normal tissue biopsy, mastectomy, blood, lymph node, serum or urine samples, or other tissue, homogenate, or extract thereof obtained from a patient.

25 There are a variety of assay formats known to those of ordinary skill in the art for using an antibody to detect polypeptide markers in a sample. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, the assay may be performed in a Western blot format, wherein a protein preparation from the biological sample is submitted to gel electrophoresis, 30 transferred to a suitable membrane and allowed to react with the antibody. The

presence of the antibody on the membrane may then be detected using a suitable detection reagent, as described below.

In another embodiment, the assay involves the use of antibody immobilized on a solid support to bind to the polypeptide and remove it from the remainder of the sample. The bound polypeptide may then be detected using a second antibody or reagent that contains a reporter group. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized antibody after incubation of the antibody with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the antibody is indicative of the reactivity of the sample with the immobilized antibody, and as a result, indicative of the concentration of polypeptide in the sample.

The solid support may be any material known to those of ordinary skill in the art to which the antibody may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose filter or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681.

The antibody may be immobilized on the solid support using a variety of techniques known to those in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the antibody, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of

antibody ranging from about 10 ng to about 1 μ g, and preferably about 100-200 ng, is sufficient to immobilize an adequate amount of polypeptide.

Covalent attachment of antibody to a solid support may also generally be achieved by first reacting the support with a bifunctional reagent that will react with 5 both the support and a functional group, such as a hydroxyl or amino group, on the antibody. For example, the antibody may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook (1991) at A12-A13).

10 In certain embodiments, the assay for detection of polypeptide in a sample is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the biological sample, such that the polypeptide within the sample are allowed to bind to the immobilized antibody. Unbound sample is then 15 removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as 20 described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20TM (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as 25 phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with breast cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least, 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of 30 ordinary skill in the art will recognize that the time necessary to achieve equilibrium

may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support 5 with an appropriate buffer, such as PBS containing 0.1% Tween 20TM. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard 10 methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed 15 and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different 20 reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of breast cancer, the signal 25 detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value established from non-tumor tissue. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients, without breast cancer. In general, a sample generating a signal that is three standard 30 deviations above the predetermined cut-off value may be considered positive for breast

cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, p. 106-7 (Little Brown and Co., 1985). Briefly, in this embodiment, the cut-off value may be determined from a plot of 5 pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered 10 positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for breast cancer.

In a related embodiment, the assay is performed in a flow-through or 15 strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, the polypeptide within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody 20 may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of breast cancer. Typically, the 25 concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that, would be sufficient to generate a positive signal in the two-antibody sandwich assay, in 30 the format discussed above. Preferably, the amount of antibody immobilized on the

membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 1 μ g. Such tests can typically be performed with a very small amount of biological sample.

The presence or absence of breast cancer in a patient may also be 5 determined by evaluating the level of mRNA encoding a breast tumor-specific polypeptide as described herein within the biological sample (e.g., a biopsy, mastectomy and/or blood sample from a patient) relative to a predetermined cut-off value. Such an evaluation may be achieved using any of a variety of methods known to those of ordinary skill in the art such as, for example, *in situ* hybridization and 10 amplification by polymerase chain reaction.

For example, polymerase chain reaction may be used to amplify sequences from cDNA prepared from RNA that is isolated from one of the above biological samples. Sequence-specific primers for use in such amplification may be 15 designed based on the sequences provided in any one of SEQ ID NO: 1, 11-86 and 142-297, and may be purchased or synthesized. In the case of B18Ag1, as noted herein, one suitable primer pair is B18Ag1-2 (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO.:126) and B18Ag1-3 (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO.:127). The PCR reaction products may then be separated by gel electrophoresis and visualized according to methods well known to those of ordinary skill in the art. 20 Amplification is typically performed on samples obtained from matched pairs of tissue (tumor and non-tumor tissue from the same individual) or from unmatched pairs of tissue (tumor and non-tumor tissue from different individuals). The amplification reaction is preferably performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the 25 tumor sample as compared to the same dilution of the non-tumor sample is considered positive.

As used herein, the term "primer/probe specific for a DNA/RNA molecule" means an oligonucleotide sequence that has at least about 80% identity 30 preferably at least about 90% and more preferably at least about 95%, identity to the DNA/RNA molecule in question. Primers and/or probes which may be usefully

employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the polymerase chain reaction primers comprise at least about 10 contiguous nucleotides of a DNA/RNA molecule encoding one of the polypeptides disclosed herein. Preferably, oligonucleotide probes for use in 5 the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA/RNA molecule encoding one of the polypeptides disclosed herein. Techniques for both PCR based assays and *in situ* hybridization assays are well known in the art.

Conventional RT-PCR protocols using agarose and ethidium bromide 10 staining while important in defining gene specificity do not lend themselves to diagnostic kit development because of the time and effort required in making them quantitative (i.e., construction of saturation and/or titration curves), and their sample throughput. This problem is overcome by the development of procedures such as real time RT-PCR which allows for assays to be performed in single tubes, and in turn can 15 be modified for use in 96 well plate formats. Instrumentation to perform such methodologies are available from Perkin Elmer/Applied Biosystems Division. Alternatively, other high throughput assays using labeled probes (e.g., digoxigenin) in combination with labeled (e.g., enzyme fluorescent, radioactive) antibodies to such probes can also be used in the development of 96 well plate assays.

20 In yet another method for determining the presence or absence of breast cancer in a patient, one or more of the breast tumor-specific polypeptides described may be used in a skin test. As used herein, a "skin test" is any assay performed directly on a patient in which a delayed-type hypersensitivity (DTH) reaction (such as swelling, reddening or dermatitis) is measured following intradermal injection of one or more 25 polypeptides as described above. Such injection may be achieved using any suitable device sufficient to contact the polypeptide or polypeptides with dermal cells of the patient, such as a tuberculin syringe or 1 mL syringe. Preferably, the reaction is measured at least 48 hours after injection, more preferably 48-72 hours.

The DTH reaction is a cell-mediated immune response, which is greater 30 in patients that have been exposed previously to a test antigen (i.e., an immunogenic

portion of a polypeptide employed, or a variant thereof). The response may be measured visually, using a ruler. In general, a response that is greater than about 0.5 cm in diameter, preferably greater than about 5.0 cm in diameter, is a positive response, indicative of breast cancer.

5 The breast tumor-specific polypeptides described herein are preferably formulated, for use in a skin test, as pharmaceutical compositions containing at least one polypeptide and a physiologically acceptable carrier, such as water, saline, alcohol, or a buffer. Such compositions typically contain one or more of the above polypeptides in an amount ranging from about 1 μ g to 100 μ g, preferably from about 10 μ g to 50 μ g
10 in a volume of 0.1 mL. Preferably, the carrier employed in such pharmaceutical compositions is a saline solution with appropriate preservatives, such as phenol and/or Tween 80TM.

In other aspects of the present invention, the progression and/or response to treatment of a breast cancer may be monitored by performing any of the above assays
15 over a period of time, and evaluating the change in the level of the response (*i.e.*, the amount of polypeptide or mRNA detected or, in the case of a skin test, the extent of the immune response detected). For example, the assays may be performed every month to every other month for a period of 1 to 2 years. In general, breast cancer is progressing in those patients in whom the level of the response increases over time. In contrast,
20 breast cancer is not progressing when the signal detected either remains constant or decreases with time.

In further aspects of the present invention, the compounds described herein may be used for the immunotherapy of breast cancer. In these aspects, the compounds (which may be polypeptides, antibodies or nucleic acid molecules) are
25 preferably incorporated into pharmaceutical compositions or vaccines. Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more polypeptides and an immune response enhancer, such as an adjuvant or a liposome (into which the compound is incorporated) Pharmaceutical compositions and vaccines may additionally contain a delivery system,
30 such as biodegradable microspheres which are disclosed, for example, in U.S. Patent

Nos. 4,897,268 and 5,075,109. Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, including one or more separate polypeptides.

Alternatively, a vaccine may contain DNA encoding one or more of the 5 polypeptides as described above, such that the polypeptide is generated *in situ*. In such vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and 10 terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication 15 competent virus. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749 (1993), and reviewed by Cohen, *Science* 259:1691-1692 (1993). The uptake of naked DNA may be increased by 20 coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a 25 wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention.

Any of a variety of adjuvants may be employed in the vaccines of this invention to nonspecifically enhance the immune response. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, 5 *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI), Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ), alum, biodegradable microspheres, monophosphoryl lipid A and quill A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also 10 be used as adjuvants.

The above pharmaceutical compositions and vaccines may be used, for example, for the therapy of breast cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with breast cancer. Accordingly, the above pharmaceutical compositions and 15 vaccines may be used to prevent the development of breast cancer or to treat a patient afflicted with breast cancer. To prevent the development of breast cancer, a pharmaceutical composition or vaccine comprising one or more polypeptides as described herein may be administered to a patient. Alternatively, naked DNA or plasmid or viral vector encoding the polypeptide may be administered. For treating a 20 patient with breast cancer, the pharmaceutical composition or vaccine may comprise one or more polypeptides, antibodies or nucleotide sequences complementary to DNA encoding a polypeptide as described herein (e.g., antisense RNA or antisense deoxyribonucleotide oligonucleotides).

Routes and frequency of administration, as well as dosage, will vary 25 from individual to individual. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered for a 52-week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given 30 periodically thereafter. Alternate protocols may be appropriate for individual patients.

A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*.

5 Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (e.g., more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about

10 100 µg to 5 mg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

PREPARATION OF BREAST TUMOR-SPECIFIC cDNAs USING
5 DIFFERENTIAL DISPLAY RT-PCR

This Example illustrates the preparation of cDNA molecules encoding breast tumor-specific polypeptides using a differential display screen.

A. Preparation of B18Ag1 cDNA and Characterization of mRNA Expression

10 Tissue samples were prepared from breast tumor and normal tissue of a patient with breast cancer that was confirmed by pathology after removal from the patient. Normal RNA and tumor RNA was extracted from the samples and mRNA was isolated and converted into cDNA using a (dT)₁₂AG (SEQ ID NO.:130) anchored 3' primer. Differential display PCR was then executed using a randomly chosen primer
15 (CTTCAACCTC) (SEQ ID NO.:103). Amplification conditions were standard buffer containing 1.5 mM MgCl₂, 20 pmol of primer, 500 pmol dNTP, and 1 unit of *Taq* DNA polymerase (Perkin-Elmer, Branchburg, NJ). Forty cycles of amplification were performed using 94°C denaturation for 30 seconds, 42°C annealing for 1 minute, and 72°C extension for 30 seconds. An RNA fingerprint containing 76 amplified products
20 was obtained. Although the RNA fingerprint of breast tumor tissue was over 98% identical to that of the normal breast tissue, a band was repeatedly observed to be specific to the RNA fingerprint pattern of the tumor. This band was cut out of a silver stained gel, subcloned into the T-vector (Novagen, Madison, WI) and sequenced.

25 The sequence of the cDNA, referred to as B18Ag1, is provided in SEQ ID NO:1. A database search of GENBANK and EMBL revealed that the B18Ag1 fragment initially cloned is 77% identical to the endogenous human retroviral element S71, which is a truncated retroviral element homologous to the Simian Sarcoma Virus (SSV). S71 contains an incomplete *gag* gene, a portion of the *pol* gene and an LTR-like structure at the 3' terminus (see Werner et al., *Virology* 174:225-238 (1990)). B18Ag1

is also 64% identical to SSV in the region corresponding to the P30 (gag) locus. B18Ag1 contains three separate and incomplete reading frames covering a region which shares considerable homology to a wide variety of gag proteins of retroviruses which infect mammals. In addition, the homology to S71 is not just within the *gag* gene, but 5 spans several kb of sequence including an LTR.

B18Ag1-specific PCR primers were synthesized using computer analysis guidelines. RT-PCR amplification (94°C, 30 seconds; 60°C → 42°C, 30 seconds; 72°C, 30 seconds for 40 cycles) confirmed that B18Ag1 represents an actual mRNA sequence present at relatively high levels in the patient's breast tumor tissue. The primers used 10 in amplification were B18Ag1-1 (CTG CCT GAG CCA CAA ATG) (SEQ ID NO.:128) and B18Ag1-4 (CCG GAG GAG GAA GCT AGA GGA ATA) (SEQ ID NO.:129) at a 3.5 mM magnesium concentration and a pH of 8.5, and B18Ag1-2 (ATG GCT ATT TTC GGG GCC TGA CA) (SEQ ID NO.:126) and B18Ag1-3 (CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO.:127) at 2 mM magnesium at pH 9.5. The same 15 experiments showed exceedingly low to nonexistent levels of expression in this patient's normal breast tissue (*see* Figure 1). RT-PCR experiments were then used to show that B18Ag1 mRNA is present in nine other breast tumor samples (from Brazilian and American patients) but absent in, or at exceedingly low levels in, the normal breast tissue corresponding to each cancer patient. RT-PCR analysis has also shown that the 20 B18Ag1 transcript is not present in various normal tissues (including lymph node, myocardium and liver) and present at relatively low levels in PBMC and lung tissue. The presence of B18Ag1 mRNA in breast tumor samples, and its absence from normal breast tissue, has been confirmed by Northern blot analysis, as shown in Figure 2.

The differential expression of B18Ag1 in breast tumor tissue was also 25 confirmed by RNase protection assays. Figure 3 shows the level of B18Ag1 mRNA in various tissue types as determined in four different RNase protection assays. Lanes 1-12 represent various normal breast tissue samples, lanes 13-25 represent various breast tumor samples; lanes 26-27 represent normal prostate samples; lanes 28-29 represent prostate tumor samples; lanes 30-32 represent colon tumor samples; lane 33 represents 30 normal aorta; lane 34 represents normal small intestine; lane 35 represents normal skin,

lane 36 represents normal lymph node; lane 37 represents normal ovary; lane 38 represents normal liver; lane 39 represents normal skeletal muscle; lane 40 represents a first normal stomach sample, lane 41 represents a second normal stomach sample; lane 42 represents a normal lung; lane 43 represents normal kidney; and lane 44 represents 5 normal pancreas. Interexperimental comparison was facilitated by including a positive control RNA of known β -actin message abundance in each assay and normalizing the results of the different assays with respect to this positive control.

RT-PCR and Southern Blot analysis has shown the B18Ag1 locus to be present in human genomic DNA as a single copy endogenous retroviral element. A 10 genomic clone of approximately 12-18 kb was isolated using the initial B18Ag1 sequence as a probe. Four additional subclones were also isolated by XbaI digestion. Additional retroviral sequences obtained from the ends of the XbaI digests of these clones (located as shown in Figure 4) are shown as SEQ ID NO:3 - SEQ ID NO:10, where SEQ ID NO:3 shows the location of the sequence labeled 10 in Figure 4, SEQ ID 15 NO:4 shows the location of the sequence labeled 11-29, SEQ ID NO:5 shows the location of the sequence labeled 3, SEQ ID NO:6 shows the location of the sequence labeled 6, SEQ ID NO:7 shows the location of the sequence labeled 12, SEQ ID NO:8 shows the location of the sequence labeled 13, SEQ ID NO:9 shows the location of the sequence labeled 14 and SEQ ID NO:10 shows the location of the sequence labeled 11- 20 22.

Subsequent studies demonstrated that the 12-18 kb genomic clone contains a retroviral element of about 7.75 kb, as shown in Figures 5A and 5B. The sequence of this retroviral element is shown in SEQ ID NO: 141. The numbered line at the top of Figure 5A represents the sense strand sequence of the retroviral genomic 25 clone. The box below this line shows the position of selected restriction sites. The arrows depict the different overlapping clones used to sequence the retroviral element. The direction of the arrow shows whether the single-pass subclone sequence corresponded to the sense or anti-sense strand. Figure 5B is a schematic diagram of the retroviral element containing B18Ag1 depicting the organization of viral genes within 30 the element. The open boxes correspond to predicted reading frames, starting with a

methionine, found throughout the element. Each of the six likely reading frames is shown, as indicated to the left of the boxes, with frames 1-3 corresponding to those found on the sense strand.

Using the cDNA of SEQ ID NO:1 as a probe, a longer cDNA was
5 obtained (SEQ ID NO:227) which contains minor nucleotide differences (less than 1%) compared to the genomic sequence shown in SEQ ID NO:141.

B. Preparation of cDNA Molecules Encoding Other Breast Tumor-Specific Polypeptides

Normal RNA and tumor RNA was prepared and mRNA was isolated and
10 converted into cDNA using a (dT)₁₂AG anchored 3' primer, as described above. Differential display PCR was then executed using the randomly chosen primers SEQ ID NO.: 87-125. Amplification conditions were as noted above, and bands observed to be specific to the RNA fingerprint pattern of the tumor were cut out of a silver stained gel, subcloned into either the T-vector (Novagen, Madison, WI) or the pCRII vector
15 (Invitrogen, San Diego, CA) and sequenced. The sequences are provided in SEQ ID NO:11 - SEQ ID NO:86. Of the 79 sequences isolated, 67 were found to be novel (SEQ ID NO.:11-26 and 28-77) (*see also* Figures 6-20).

An extended DNA sequence (SEQ ID NO: 290) for the antigen B15Ag1 (originally identified partial sequence provided in SEQ ID NO: 27) was obtained in
20 further studies. Comparison of the sequence of SEQ ID NO: 290 with those in the gene bank as described above, revealed homology to the known human β -A activin gene.

Subsequent studies identified an additional 146 sequences (SEQ ID NOS:142-289), of which 115 appeared to be novel (SEQ ID NOS:142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-
25 240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291). To the best of the inventors' knowledge none of the previously identified sequences have heretofore been shown to be expressed at a greater level in human breast tumor tissue than in normal breast tissue.

In further studies, six different splice forms of the antigen B11Ag1 were
30 isolated, with each of the various splice forms containing slightly different versions of

the B11Ag1 coding frame. Splice junction sequences define individual exons which, in various patterns and arrangements, make up the various splice forms. Primers were designed to examine the expression pattern of each of the exons using RT-PCR as described below. Each exon was found to show the same expression pattern as the 5 original B11Ag1 clone, with expression being breast tumor, prostate and testis-specific. The determined cDNA sequences for the isolated protein coding exons are provided in SEQ ID NO: 292-297, respectively.

EXAMPLE 2

10

PREPARATION OF B18Ag1 DNA FROM HUMAN GENOMIC DNA

This Example illustrates the preparation of B18Ag1 DNA by amplification from human genomic DNA.

B18Ag1 DNA may be prepared from 250 ng human genomic DNA 15 using 20 pmol of B18Ag1 specific primers, 500 pmol dNTPS and 1 unit of *Taq* DNA polymerase (Perkin Elmer, Branchburg, NJ) using the following amplification parameters: 94°C for 30 seconds denaturing, 30 seconds 60°C to 42°C touchdown annealing in 2°C increments every two cycles and 72°C extension for 30 seconds. The last increment (a 42°C annealing temperature) should cycle 25 times. Primers were 20 selected using computer analysis. Primers synthesized were B18Ag1-1, B18Ag1-2, B18Ag1-3, and B18Ag1-4. Primer pairs that may be used are 1+3, 1+4, 2+3, and 2+4.

Following gel electrophoresis, the band corresponding to B18Ag1 DNA may be excised and cloned into a suitable vector.

25

EXAMPLE 3

PREPARATION OF B18Ag1 DNA FROM BREAST TUMOR cDNA

This Example illustrates the preparation of B18Ag1 DNA by amplification from human breast tumor cDNA.

First strand cDNA is synthesized from RNA prepared from human breast tumor tissue in a reaction mixture containing 500 ng poly A+ RNA, 200 pmol of the primer (T)₁₂AG (*i.e.*, TTT TTT TTT TTT AG) (SEQ ID NO: 130), 1X first strand reverse transcriptase buffer, 6.7 mM DTT, 500 mmol dNTPs, and 1 unit AMV or 5 MMLV reverse transcriptase (from any supplier, such as Gibco-BRL (Grand Island, NY)) in a final volume of 30 μ l. After first strand synthesis, the cDNA is diluted approximately 25 fold and 1 μ l is used for amplification as described in Example 2. While some primer pairs can result in a heterogeneous population of transcripts, the primers B18Ag1-2 (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO: 126) 10 and B18Ag1-3 (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO: 127) yield a single 151 bp amplification product.

EXAMPLE 4

IDENTIFICATION OF B-CELL AND T-CELL EPITOPES OF B18Ag1

15

This Example illustrates the identification of B18Ag1 epitopes.

The B18Ag1 sequence can be screened using a variety of computer algorithms. To determine B-cell epitopes, the sequence can be screened for hydrophobicity and hydrophilicity values using the method of Hopp, *Prog. Clin. Biol. Res.* 172B:367-77 (1985) or, alternatively, Cease et al., *J. Exp. Med.* 164:1779-84 (1986) or Spouge et al., *J. Immunol.* 138:204-12 (1987). Additional Class II MHC (antibody or B-cell) epitopes can be predicted using programs such as AMPHI (*e.g.*, Margalit et al., *J. Immunol.* 138:2213 (1987)) or the methods of Rothbard and Taylor (*e.g.*, *EMBO J.* 7:93 (1988)).

25

Once peptides (15-20 amino acids long) are identified using these techniques, individual peptides can be synthesized using automated peptide synthesis equipment (available from manufacturers such as Perkin Elmer/Applied Biosystems Division, Foster City, CA) and techniques such as Merrifield synthesis. Following, synthesis, the peptides can be used to screen sera harvested from either normal or breast 30 cancer patients to determine whether patients with breast cancer possess antibodies

reactive with the peptides. Presence of such antibodies in breast cancer patient would confirm the immunogenicity of the specific B-cell epitope in question. The peptides can also be tested for their ability to generate a serologic or humoral immune in animals (mice, rats, rabbits, chimps etc.) following immunization *in vivo*. Generation of a 5 peptide-specific antiserum following such immunization further confirms the immunogenicity of the specific B-cell epitope in question.

To identify T-cell epitopes, the B18Ag1 sequence can be screened using different computer algorithms which are useful in identifying 8-10 amino acid motifs within the B18Ag1 sequence which are capable of binding to HLA Class I MHC 10 molecules. (see, e.g., Rammensee et al., *Immunogenetics* 41:178-228 (1995)). Following synthesis such peptides can be tested for their ability to bind to class I MHC using standard binding assays (e.g., Sette et al., *J. Immunol.* 153:5586-92 (1994)) and more importantly can be tested for their ability to generate antigen reactive cytotoxic T-cells following *in vitro* stimulation of patient or normal peripheral mononuclear cells 15 using, for example, the methods of Bakker et al., *Cancer Res.* 55:5330-34 (1995); Visseren et al., *J. Immunol.* 154:3991-98 (1995); Kawakami et al., *J. Immunol.* 154:3961-68 (1995); and Kast et al., *J. Immunol.* 152:3904-12 (1994). Successful *in vitro* generation of T-cells capable of killing autologous (bearing the same Class I MHC molecules) tumor cells following *in vitro* peptide stimulation further confirms the 20 immunogenicity of the B18Ag1 antigen. Furthermore, such peptides may be used to generate murine peptide and B18Ag1 reactive cytotoxic T-cells following *in vivo* immunization in mice rendered transgenic for expression of a particular human MHC Class I haplotype (Vitiello et al., *J. Exp. Med.* 173:1007-15 (1991)).

A representative list of predicted B18Ag1 B-cell and T-cell epitopes, 25 broken down according to predicted HLA Class I MHC binding antigen, is shown below:

Predicted Th Motifs (B-cell epitopes) (SEQ ID NOS.: 131-133)

SSGGRTFDDFHRYLLVGI

SPGVFLEHLQEAYRIYTPFDLSA

Predicted HLA A2.1 Motifs (T-cell epitopes) (SEQ ID NOS.: 134-140)

YLLVGIQGA
5 GAAQKPINL
NLSKXIEVV
EVVQGHDES
HLQEAYRIY
NLAFAVAAQAA
10 FVAQAAPDS

EXAMPLE 5

CHARACTERIZATION OF BREAST TUMOR GENES DISCOVERED BY
DIFFERENTIAL DISPLAY PCR

15

The specificity and sensitivity of the breast tumor genes discovered by differential display PCR were determined using RT-PCR. This procedure enabled the rapid evaluation of breast tumor gene mRNA expression semiquantitatively without using large amounts of RNA. Using gene specific primers, mRNA expression levels in 20 a variety of tissues were examined, including 8 breast tumors, 5 normal breasts, 2 prostate tumors, 2 colon tumors, 1 lung tumor, and 14 other normal adult human tissues, including normal prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach and testes.

To ensure the semiquantitative nature of the RT-PCR, β -actin was used 25 as internal control for each of the tissues examined. Serial dilutions of the first strand cDNAs were prepared and RT-PCR assays performed using β -actin specific primers. A dilution was then selected that enabled the linear range amplification of β -actin template, and which was sensitive enough to reflect the difference in the initial copy number. Using this condition, the β -actin levels were determined for each reverse 30 transcription reaction from each tissue. DNA contamination was minimized by DNase

treatment and by assuring a negative result when using first strand cDNA that was prepared without adding reverse transcriptase.

Using gene specific primers, the mRNA expression levels were determined in a variety of tissues. To date, 38 genes have been successfully examined 5 by RT-PCR, five of which exhibit good specificity and sensitivity for breast tumors (B15AG-1, B31GA1b, B38GA2a, B11A1a and B18AG1a). Figures 21A and 21B depict the results for three of these genes: B15AG-1 (SEQ ID NO:27), B31GA1b (SEQ ID NO:148) and B38GA2a (SEQ ID NO. 157). Table I summarizes the expression level of all the genes tested in normal breast tissue and breast tumors, and also in other 10 tissues.

TABLE I

Percentage of Breast Cancer Antigens that are Expressed in Various Tissues

15	Breast Tissues	Over-expressed in Breast Tumors	84%
		Equally Expressed in Normals and Tumor	16%
20		Over-expressed in Breast Tumors but <u>not in any Normal Tissues</u>	9%
25	Other Tissues	Over-expressed in Breast Tumors but Expressed in Some Normal Tissues	30%
		Over-expressed in Breast Tumors but Equally Expressed in All Other Tissues	61%

30 From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Frudakis, Tony N.
Smith, John M.
Reed, Steven G.

(ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER

(iii) NUMBER OF SEQUENCES: 297

(iv) CORRESPONDENCE ADDRESS:

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- (B) STREET: 6300 Columbia Center, 701 Fifth Avenue
- (C) CITY: Seattle
- (D) STATE: Washington
- (E) COUNTRY: USA
- (F) ZIP: 98104-7092

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE: 04-APR-1997
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Maki, David J.
- (B) REGISTRATION NUMBER: 31,392
- (C) REFERENCE/DOCKET NUMBER: 210121.419C2

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (206) 622-4900
- (B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTA GAG ACC CAA TTG GGA CCT AAT TGG GAC CCA AAT TTC TCA AGT GGA	48
Leu Glu Thr Gln Leu Gly Pro Asn Trp Asp Pro Asn Phe Ser Ser Gly	
1 5 10 15	
GGG AGA ACT TTT GAC GAT TTC CAC CGG TAT CTC CTC GTG GGT ATT CAG	96
Gly Arg Thr Phe Asp Asp Phe His Arg Tyr Leu Leu Val Gly Ile Gln	
20 25 30	
GGA GCT GCC CAG AAA CCT ATA AAC TTG TCT AAG GCG ATT GAA GTC GTC	144
Gly Ala Ala Gln Lys Pro Ile Asn Leu Ser Lys Ala Ile Glu Val Val	
35 40 45	
CAG GGG CAT GAT GAG TCA CCA GGA GTG TTT TTA GAG CAC CTC CAG GAG	192
Gln Gly His Asp Glu Ser Pro Gly Val Phe Leu Glu His Leu Gln Glu	
50 55 60	
GCT TAT CGG ATT TAC ACC CCT TTT GAC CTG GCA GCC CCC GAA AAT AGC	240
Ala Tyr Arg Ile Tyr Thr Pro Phe Asp Leu Ala Ala Pro Glu Asn Ser	
65 70 75 80	
CAT GCT CTT AAT TTG GCA TTT GTG GCT CAG GCA GCC CCA GAT AGT AAA	288
His Ala Leu Asn Leu Ala Phe Val Ala Gln Ala Ala Pro Asp Ser Lys	
85 90 95	
AGG AAA CTC CAA AAA CTA GAG GGA TTT TGC TGG AAT GAA TAC CAG TCA	336
Arg Lys Leu Gln Lys Leu Glu Gly Phe Cys Trp Asn Glu Tyr Gln Ser	
100 105 110	
GCT TTT AGA GAT AGC CTA AAA GGT TTT	363
Ala Phe Arg Asp Ser Leu Lys Gly Phe	
115 120	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Glu Thr Gln Leu Gly Pro Asn Trp Asp Pro Asn Phe Ser Ser Gly	
1 5 10 15	
Gly Arg Thr Phe Asp Asp Phe His Arg Tyr Leu Leu Val Gly Ile Gln	
20 25 30	
Gly Ala Ala Gln Lys Pro Ile Asn Leu Ser Lys Ala Ile Glu Val Val	
35 40 45	
Gln Gly His Asp Glu Ser Pro Gly Val Phe Leu Glu His Leu Gln Glu	
50 55 60	
Ala Tyr Arg Ile Tyr Thr Pro Phe Asp Leu Ala Ala Pro Glu Asn Ser	

65	70	75	80
His Ala Leu Asn Leu Ala Phe Val Ala Gln Ala Ala Pro Asp Ser Lys			
85	90	95	
Arg Lys Leu Gln Lys Leu Glu Gly Phe Cys Trp Asn Glu Tyr Gln Ser			
100	105	110	
Ala Phe Arg Asp Ser Leu Lys Gly Phe			
115	120		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCTTAGAATC	TTCATACCCC	GAACCTTTGG	GAAAACTTTA	ATCAGTCACC	TACAGTCTAC	60
CACCCATTAA	GGAGGAGCAA	AGCTACCTCA	GCTCCTCCGG	AGCCGTTTTA	AGATCCCCCA	120
TCTTCAAAGC	CTAACAGATC	AAGCAGCTCT	CCGGTGCACA	ACCTGCGCCC	AGGTAAATGC	180
CAAAAAAAGGT	CCTAAACCCA	GCCCAGGCCA	CCGTCTCCAA	GAAAACTCAC	CAGGAGAAAA	240
GTGGGAAATT	GACTTTACAG	AAGTAAAACC	ACACCGGGCT	GGGTACAAAT	ACCTTCTAGT	300
ACTGGTAGAC	ACCTTCTCTG	GATGGACTGA	AGCATTGCT	ACCAAAAACG	AAACTGTCAA	360
TATGGTAGTT	AAGTTTTAC	TCAATGAAAT	CATCCCTCGA	CGTGGGCTGC	CTGTTGCCAT	420
AGGGTCTGAT	AATGGAACGG	CCTTCGCCTT	GTCTATAGTT	TAATCAGTCA	GTAAGGCCGT	480
AAACATTCAA	TGGAAGCTCC	ATTGTGCCTA	TCGACCCAGA	GCTCTGGCA	AGTAGAACGC	540
ATGAACTGCA	CCCTAAAAAA	ACACTCTTAC	AAAATTAATC	TTAAAAAACG	GTGTTAATTG	600
TGTTAGTCTC	CTTCCCTTAG	CCCTACTTAG	AGTTAAGGTG	CACCCCTTAC	TGGGCTGGGT	660
TCTTACCTT	TTGAAATCAT	NTTNNGGAAG	GGGCTGCCTA	TCTTNTCTTA	ACTAAAAAAN	720
GCCCATTTGG	CAAAAATTTC	NCAACTAATT	TNTACGTNCC	TACGTCTCCC	CAACAGGTAN	780
AAAAATCTNC	TGCCCTTTTC	AAGGAACCAT	CCCATCCATT	CCTNAACAAA	AGGCCTGCCN	840
TTCTTCCCCC	AGTTAACTNT	TTTTTNTTAA	AATTCCAAA	AAANGAACCN	CCTGCTGGAA	900
AAACNCCCCC	CTCCAANCCC	CGGCCNAAGN	GGAAAGGTTCC	CTTGAATCCC	NCCCCNCNA	960
ANGGCCCGGA	ACCNTTAAAN	TNGTCCNGG	GGGTNNGGCC	TAAAAGNCCN	ATTGGTAAA	1020
CCTANAAAATT	TTTTCTTTTN	AAAAAACAC	NNTTNNNTT	TTCTTAAACA	AAACCCCTNTT	1080
TNTAGNANCN	TATTCCCCNC	C				1101

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1087 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCTAGAGCTG	CGCCTGGATC	CCGCCACAGT	GAGGAGACCT	GAAGACCAGA	GAAAACACAG	60
CAAGTAGGGCC	CTTTAAACTA	CTCACCTGTG	TTGTCTCTA	ATTTATTCTG	TTTTATTGTTG	120
TTTCCATCAT	TTTAAGGGGT	TAAAATCATC	TTGTTCAGAC	CTCAGCATAT	AAAATGACCC	180
ATCTGTAGAC	CTCAGGCTCC	AACCATAACCC	CAAGAGTTGT	CTGGTTTGT	TTAAATTACT	240
GCCAGGTTTC	AGCTGCAGAT	ATCCCTGGAA	GGAAATATTCC	AGATCCCTG	AGTAGTTTCC	300

AGGTTAAAAT CCTATAGGCT TCTTCTGTT TGAGGAAGAG TTCCCTGTCAG AGAAAAAACAT	360
GATTTTGAT TTTAACTTT AATGCTTGTG AAACGCTATA AAAAAAAATT TCTACCCCTA	420
GCTTTAAAGT ACTGTTAGTG AGAAATTAAA ATTCCCTTCAG GAGGATTAAA CTGCCATTTC	480
AGTTACCCCA ATTCCAAATG TTTTGGTGGT TAGAATCTTC TTTAATGTT TTGAAGAAGT	540
GTTTTATATT TTCCCACATCNA GATAAAATTCT CTCNCNCCTT NNNTTTNTNT CTNNNTTTTT	600
AAAACGGANT CTTGCTCCGT TGTCCANGCT GGGAAATTNTN TTTTGGCCAA TCTCCGCTNC	660
CTTGCAANAA TNCTGCNTCC CAAAATTACC NCCTTTTCC CACCTCCACC CCNNNGGAATT	720
ACCTGGAATT ANAGGGCCCCC NCCCCCCCCC CGGCTAATTG GTTTTGTGTT TTAGTAAAAA	780
ACGGGTTTCC TGTTTAGTT AGGATGGCCC ANNTCTGACC CCNTNATCNT CCCCCCTCNGC	840
CCTCNAATNT TNNGNNTANG GCTTACCCCC CCCNGNNGTT TTTCTCCAT TNAAATTTC	900
TNTGGANTCT TGAATNNCGG GTTTCCCTT TTAAACCNAT TTTTTTTTN NNNCCCCCAN	960
TTTNCCTCC CCCNTNTNTA ANGGGGTTT CCCAANCCGG GTCCNCCCCC ANGTCCCCAA	1020
TTTTCTCCC CCCCCCTCTT TTTCTTTNC CCCAAAANTC CTATCTTTC CTNNAAATAT	1080
CNANTNT	1087

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCTAGACCAA GAAATGGGAG GATTTAGAG TGACTGATGAA TTTCTCTATC ATCTGCAGTT	60
AGTAAACATT CTCCACAGTT TATGAAAAA GTAACAAAAC CACTGCAGAT GACAAACACT	120
AGGTAACACA CATACTATCT CCCAAATACC TACCCACAAG CTCAACAATT TTAAACTGTT	180
AGGATCACTG GCTCTAATCA CCATGACATG AGGTCACCAC CAAACCATCA AGCGCTAAC	240
AGACAGAATG TTTCCACTCC TGATCCACTG TGTTGGAAAGA AGCACCGAAC TTACCCACTG	300
GGGGGCCTGC NTCANAANAA AAGCCCATGC CCCCGGGTNT NCCTTNAAC CGGAACGAAT	360
NAACCCACCA TCCCCACANC TCCTCTGTTC NTGGGCCCTG CATCTGTGG CCTCNTNTNC	420
TTTNGGGGAN ACNTGGGAA GGTACCCAT TTCNTTGACC CCNCNANAAA ACCCCNGTGG	480
CCCTTTGCC TGATTCNCNT GGGCCTTTTC TCTTTTCCCT TTTGGGTTGT TTAAATTCCC	540
AATGTCCCCN GAACCCTCTC CNTNCTGCC AAAACCTACC TAAATTNCTC NCTANGNNT	600
TTCTTGGGTG TNCTTTCAA AGGTNACCTT NCCTGTTCAN NCCCNACNAA AATTNTTCC	660
NTATNNTGGN CCCNAAAAAA NNNATCNNCC CNAATTGCC GAATTGGTTN GGTTTTCC	720
NCTGGGGAA ACCCTTTAAA TTTCCCCCTT GGGCGGCCCC CCTTTTTCC CCCCTTNGA	780
AGGCAGGNNG TTCTTCCCGA ACTTCCAATT NCAACAGCCN TGCCCATTGN TGAAACCC	840
TTCCTAAAAT TAAAAAATAN CCGGTTNNGG NNNGCCTCTT TCCCCCTCCNG GNNGGNNGNG	900
AAANTCCTTA CCCCCAAAAA GGTTGCTTAG CCCCCNGTCC CCACTCCCCC NGGAAAAATN	960
AACCTTTCTN AAAAAGGAA TATAANTTN CCACTCCTTN GTTCTCTTCC	1010

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 950 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCTAGAGCTC GCGGCCGCGA GCTCTAATAC GACTCACTAT AGGGCGTCGA CTCGATCTCA	60
GCTCACTGCA ATCTCTGCC CCGGGGTCA GCGATTCTCC TGCCCTCAGCC TTCCAAGTAG	120
CTGGGATTAC AGGCGTCAA CACCACACCC GGCTAATTAA GTATTTTAA TAGAGATGGG	180
GTTTCCCTT GTTGGCCANN ATGGTCTCNA ACCCCTGACC TCNNNGTGATC CCCCCNCCCN	240
NGANCTCNNA CTGCTGGGA TNNCGGNNNN NNNCCTCCCN NCNCNNNNNN NCNCNNTCCN	300
TNNTCCTNC TCNNNNNNNN CNNTCNTCC NNCTTCTCNC CNNNTTTNT CNNCNCCNN	360
CNNNCCNCNT NCCCNCCNNN TCNCNTNCNN TNTCCNNNN NNTCCNNNN CNNNCNTNN	420
CCNNTACNTC NTNNNCNNNT CCNTCTNTNN CCTCCNNNTN CNCTNCNCNT TNTCTCCTCN	480
NTNNNNNNCT CCNNNNNTCT CNTCNCNCN TNCCCTCNCN NCCNCNCNC NCCTCNCNN	540
CTNNTTTNNN CNNCNNTCC NTNCCNTCN NNTCCNNNTN CNNCNCNCN NNCNTTNTTC	600
CCNCCNNNTC CTTNCNCNTN NNNNTCNCN CNCNCNNNTC NTTTNCTCCT NNNTCCNNC	660
TCNNTTCNCC CNNNTCCNCC CCCCNCNTN CTCTCNCNN NNTNNNTNTN NNNCNTCCNC	720
TNTCNCNTTC NTCNNTNCNT TNCTNCNNC NNCCNTNCNC TNCCNTNTNT CTNNNTCNCN	780
TCNCNTNTCN CCNTCCNTN CTNTCTCCTN TNTCCTCCTC CTCNCCTNCT CNTTCNCNC	840
CCNNTNTNTN TNNCNCCNNT NCTNNNCNNC CNTCNTTCN TCTCTNCTNN NNNTNNCCTC	900
NNCCNNTNCC CTNNNTNCNT NCTNNTACCN TNCTNCTCN TCTTCCTTCC	950

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1086 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCTAGAGCTC GCGGCCGCGA GCTCAATTAA CCCTCACTAA AGGGAGTCGA CTCGATCAGA	60
CTGTTACTGT GTCTATGTAG AAAGAAGTAG ACATAAGAGA TTCCATTTCG TTCTGTACTA	120
AGAAAAATTC TTCTGCCTTG AGATGCTGTT AATCTGTAAC CCTAGCCCCA ACCCTGTGCT	180
CACAGAGACA TGTGCTGTG TGACTCAAGG TTCAATGGAT TTAGGGCTAT GCTTGTAA	240
AAAAGTGCTT GAAGATAATA TGCTTGTAA AAGTCATCAC CATTCTCTAA TCTCAAGTAC	300
CCAGGGACAC AATACACTGC GGAAGGCCGC AGGGACCTCT GTCTAGGAAA GCCAGGTATT	360
GTCCAAGATT TCTCCCCATG TGATAGCCTG AGATATGGCC TCATGGGAAG GGTAAGACCT	420
GACTGTCCCC CAGCCCGACA TCCCCCAGCC CGACATCCCC CAGCCCGACA CCCGAAAAGG	480
GTCTGTGCTG AGGAAGATTA NTAAAAGAGG AAGGCTCTTT GCATTGAAGT AAGAAGAAGG	540
CTCTGTCTCC TGCTCGTCCC TGGGCAATAA AATGTCTTGG TGTAAACCC GAATGTATGT	600
TCTACTTACT GAGAATAGGA GAAAACATCC TTAGGGCTGG AGGTGAGACA CCCTGGCGGC	660
ATACTGCTCT TTAATGCACG AGATGTTGT NTAATTGCCA TCCAGGGCCA NCCCCTTTCC	720
TTAACCTTTT ATGANACAAA AACTTGTTC NCTTTCTTG CGAACCTCTC CCCCTATTAN	780
CCTATTGGCC TGCCCCATCCC CTCCCCAAAN GGTGAAAANA TGTCNTAAA TNCGAGGGAA	840
TCCAAAACNT TTTCCCGTTG GTCCCCTTTC CAACCCCGTC CCTGGGCCNN TTTCTCCCC	900
AACNTGTCCC GGNTCCTTCN TTCCCNCCCC CTTCCNGAN AAAAAACCCC GTNTGANGGN	960
GCCCCCTCAA ATTATAACCT TTCCNAACAA AANNGTTCN AAGGTGGTTT GNNTCCGGTG	1020
CGGCTGGCCT TGAGGTCCCC CCTNCACCCCC AATTGGAAN CCNGTTTTT TTATTGCCCN	1080
NTCCCC	1086

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

NCCNTTTAGA	TGTTGACAAN	NTAAACAAGC	NGCTCAGGCA	GCTGAAAAAA	GCCACTGATA	60
AAGCATCCTG	GAGTATCAGA	GTTTACTGTT	AGATCAGCCT	CATTGACTT	CCCCCTCCAC	120
ATGGTGTAA	AATCCAGCTA	CACTACTTCC	TGACTCAAAC	TCCACTATT	CTGTTCATGA	180
CTGTCAGGAA	CTGTTGGAAA	CTACTGAAAC	TGGCCGACCT	GATCTCAAA	ATGTGCCCT	240
AGGAAAGGTG	GATGCCACCG	TGTTCACAGA	CAGTACCNCC	TTCCTCGAGA	AGGGACTACG	300
AGGGGCCGT	GCANCTGTTA	CCAAGGAGAC	TNATGTGTTG	TGGGCTCAGG	CTTTACCANC	360
AAACACCTCA	NCNCNNAAGG	CTGAATTGAT	CGCCCTCACT	CAGGCTCTCG	GATGGGGTAA	420
GGGATATTAA	CGTTAACACT	GACAGCAGGT	ACGCCTTGC	TACTGTGCAT	GTACGTGGAG	480
CCATCTACCA	GGAGCGTGGG	CTACTCACTC	GGCAGGTGGC	TGTNATCCAC	TGTAAANGGA	540
CATCAAAGG	AAAACNNNGG	TGTTGCCGT	GTAAACCANA	AANCTGATCN	NCAGCTCNAA	600
GATGCTGTGT	TGACTTTCAC	TCNCNCTCT	TAACACTTGCT	GCCCACANTC	TCCTTCCCA	660
ACCAGATCTG	CCTGACAATC	CCCATACTCA	AAAAAAAAN	AAANACTGGCC	CCGAACCCNA	720
ACCAATAAAA	ACGGGGANGG	TNGGTNGANC	NNCCTGACCC	AAAATAATG	GATCCCCCGG	780
GCTGCAGGAA	TTCAATTCAN	CCTTATCNAT	ACCCCCAACN	NGGNGGGGGG	GGCCNGTNCC	840
CATTNCCCT	NTATTNATT	TTTNNCCCCC	CCCCCGGCNT	CCTTTTNAA	CTCGTAAAG	900
GGAAAACCTG	NCTTACCAAN	TTATCNCTG	GACCNTCCCC	TTCCNCGGTN	GNTTANAAAA	960
AAAAGCCNC	ANTCCNTCC	NAAATTGCA	CNGAAAGGNA	AGGAATTAA	CCTTTATTT	1020
TTNNTCCTT	ANTTGTNNN	CCCCCTTTA	CCCAAGGCAGA	CNGCCATCNT	TTAANAAAAA	1080
AAANAGAANG	TTTATTTTTC	CTTNGAACCA	TCCCAATANA	AANCACCCGC	NGGGAACGG	1140
GGNGGNAGGC	CNCTCACCCC	CTTTNTGTNG	GNNGGNC			1177

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

NCCNNNTNN	GATGTTGTCT	TTTGGCCTC	TCTTTGGATA	CTTCCCTCT	CTTCAGAGGT	60
GAAAAGGGTC	AAAAGGAGCT	GTTGACAGTC	ATCCCAGGTG	GGCCAATGTG	TCCAGAGTAC	120
AGACTCCATC	AGTGAGGTCA	AAGCCTGGGG	CTTTTCAGAG	AAGGGAGGAT	TATGGGTTTT	180
CCAATTATAC	AAGTCAGAAG	TAGAAAGAAG	GGACATAAAC	CAGGAAGGGG	GTGGAGCACT	240
CATCACCCAG	AGGGACTTGT	GCCTCTCTCA	GTGGTAGTAG	AGGGGCTACT	TCCTCCCACC	300
ACGGTTGCAA	CCAAGAGGCA	ATGGGTGATG	AGCCTACAGG	GGACATANCC	GAGGAGACAT	360
GGGATGACCC	TAAGGGAGTA	GGCTGGTTT	AAGGCGGTGG	GACTGGGTGA	GGGAAACTCT	420
CCTCTTCTTC	AGAGAGAACG	AGTACAGGGC	GAGCTGAACC	GGCTGAAGGT	CGAGGCGAAA	480
ACACGGCTCG	GCTCAGGAAG	ACCTTGAAG	TAAAATTATG	AATGGTGCAT	GAATGGAGCC	540
ATGGAAGGGG	TGCTCCTGAC	CAAACCTCAGC	CATTGATCAA	TGTTAGGGAA	ACTGATCAGG	600
GAAGCCGGGA	ATTCATTAA	CAACCCGCA	CACAGCTTGA	ACATTGTGAG	GTTCAGTGAC	660
CCTTCAAGGG	GCCACTCCAC	TCCAATTG	GCCATTCTAC	TTTGCNAAT	TTCCAAAAT	720
TCCTTTTTA	AGGCCGAATC	CNTANTCCCT	NAAAAACNAA	AAAAAATCTG	CNCCTATTCT	780
GGAAAAGGCC	CANCCCTTAC	CAGGCTGGAA	GAAATTTNC	CTTTTTTTT	TTTTGAAGG	840
CNTTTNTTAA	ATTGAACCTN	AATTCNCCCC	CCCAAAAAAA	AACCCNCCNG	GGGGCGGGAT	900
TTCCAAAAC	NAATTCCCTT	ACCAAAAAAC	AAAAACCCNC	CCTTNTTCCC	TTCCNCCCTN	960
TTCTTTAAT	TAGGGAGAGA	TNAAGCCCC	CAATTCCNG	GNCTNGATNN	TTTCCCCCCC	1020
CCCCCATT	CCNAAACTTT	TTCCCANCNA	GGAANCCNCC	CTTTTTTNG	GTCNGATTNA	1080
NCAACCTTCC	AAACCATT	TCCNAAAAAA	NTTGNTNGG	NGGGAAAAAN	ACCTNNNTTT	1140

ATAGAN

1146

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTTCATTGGG TACGGGCCCC CTCGAGGTCTG ACGGTATCGA TAAGCTTGAT ATCGAATTCC	60
TGCAGCCGG GGGATCCACT AGTTCTAGAG TCAGGAAGAA CCACCAACCT TCCTGATTT	120
TATTGGCTCT GAGTTCTGAG GCCAGTTTC TTCTTCTGTT GAGTATGCGG GATTGTCAGG	180
CAGATCTGGC TGTGGAAAGG AGACTGTGGG CAGCAAGTTT AGAGGCGTGA CTGAAAGTCA	240
CACTGCATCT TGAGCTGCTG AATCAGCTT CTGGTTACCA CGGGCAACAG CCGTGTTTC	300
CTTTTGATGT CCTTTACAGT GGATTACAGC CACCTGCTGA GGTGAGTAGC CCACGCTCCT	360
GGTAGATGGC TCCACGTACA TGCACAGTAG CAAAGGCGTA CCTGCTGTCA GTGTTAACGT	420
TAATATCCTT ACCCCATCGG AGAGCCTGAG TGAGGGCGAT CAATTCAAGCC CTTTTGTGCT	480
GAGGTGTTTG CTGGTTAACGC CCTGAACCCA CAACACATCT GTCTCCATGG TAACAGCTGC	540
ACCGG	545

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCTCCTAGGC TGGGCACAGT GGCTCATACC TGTAATCCTG ACCGTTTCAG AGGCTCAGGT	60
GGGGGGATCG CTTGAGCCCA AGATTTCAAG ACTAGTCTGG GTAACATAGT GAGACCCAT	120
CTCTACGAAA AAATAAAAAAA ATGAGCCTGG TGTAGTGGCA CACACCAGCT GAGGAGGGAG	180
AATCGAGCCT AGGAGA	196

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCTCCTAGGC TTGGGGGCTC TGACTAGAAA TTCAAGGAAC CTGGGATTCA AGTCCAAC	60
TGACACCAAC TTACACTGTG GNCTCCAATA AACTGCTTCT TTCCTATTCC CTCTCTATT	120
AATAAAATAA GGAAAACGAT GTCTGTGTAT AGCCAAGTCA GNTATCCTAA AAGGAGATAC	180
TAAGTGACAT TAAATATCAG AATGTAAAAC CTGGGAACCA GGTTCCCAGC CTGGGATTAA	240

ACTGACAGCA AGAAGACTGA ACAGTACTAC TGTGAAAAGC CCGAAGNGGC AATATGTTCA	300
CTCTACCGTT GAAGGGATGGC TGGGAGAATG AATGCTCTGT CCCCCAGTCC CAAGCTCACT	360
TACTATACCT CCTTTATAGC CTAGGAGA	388

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TAGTAGTTGC CTATAATCAT GTTTCTCATT ATTTCACAT TTTATTAACC AATTTCTGTT	60
TACCCCTGAAA AATATGAGGG AAATATATGA AACAGGGAGG CAATGTCAG ATAATTGATC	120
ACAAGATATG ATTTCTACAT CAGATGCTCT TTCCCTTCCT GTTTATTTCC TTTTTATTT	180
GGTTGTGGGG TCGAATGTAA TAGCTTGTT TCAAGAGAGA GTTTGGCAG TTTCTGTAGC	240
TTCTGACACT GCTCATGTCT CCAGGCATCT ATTTGCACTT TAGGAGGTGT CGTGGGAGAC	300
TGAGAGGTCT ATTTTTCCA TATTGGGCA ACTACTA	337

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TAGTAGTTGC CATAACAGTGC CTTTCCATT ATTAAACCCC CACCTGAACG GCATAAACTG	60
AGTGTTCAGC TGGTGTAAAA TACTGTAAAC AATAAGGAGA CTTTGCTCTT CATTAAACC	120
AAAATCATAT TTCAATTTT ACGCTCGAGG GTTTTACCG GTTCCCTTTT ACACTCCTTA	180
AAACAGTTT TAAGTCGTTT GGAACAAGAT ATTTTTCTT TCCTGGCAGC TTTAACATT	240
ATAGCAAATT TGTGTCTGGG GGACTGCTGG TCACTGTTTC TCACAGTTGC AAATCAAGGC	300
ATTTGCAACC AAGAAAAAAA AATTTTTTG TTTTATTGAA AACTGGACCG GATAAACGGT	360
GTTTGGAGCG GCTGCTGTAT ATAGTTTAA ATGGTTTATT GCACCTCCTT AAGTTGCACT	420
TATGTGGGGG GGGGNTTTTG NATAGAAAGT NTTTANTCAC ANAGTCACAG GGACTTTNT	480
CTTTTGGNNNA CTGAGCTAAA AAGGGCTGNT TTTGGGTGG GGGCAGATGA AGGCTCACAG	540
GAGGCCTTTC TCTTAGAGGG GGGAACTNCT A	571

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TATATATTTA ATAACCTAAA TATATTTGA TCACCCACTG GGGTGATAAG ACAATAGATA	60
TAAAAGTATT TCCAAAAGC ATAAAACCAA AGTATCATAAC CAAACCAAAT TCATACTGCT	120
TCCCCCACCC GCACGTGAAAC TTCACCTTCT AACTGTCTAC CTAACCAAAT TCTACCCCTC	180
AAGTCTTG GCGTGTCTCA CTACTCTTTT TTTTTTTTTT TTTNTTTGG AGATGGAGTC	240
TGGCTGTGCA GCCCAGGGGT GGAGTACAAT GGACACAACCT CAGCTCACTG NAACCTCCGC	300
CTCCCAGGTT CATGAGATT TCCTGNTTCA GCCTTCCCAG TAGCTGGGAC TACAGGTGTG	360
CATCACCATG CCTGGNTAAT CTTTTTNGT TTTNGGGTAG AGATGGGGT TTTACATGTT	420
GGCCAGGNTG GTNTCGAACT CCTGACCTCA AGTGATCCAC CCACCTCAGG CTCCCAAAGT	480
GCTAGGATTA CAGACATGAG CCACTGNGCC CAGNCCTGGT GCATGCTCAC TTCTCTAGGC	540
AACTACTA	548

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 638 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTCCGTTATG CACATGCAGA ATATTCTATC GGTACTTCAG CTATTACTCA TTTTGATGGC	60
GCAATCCGAG CCTATCCTCA AGATGAGTAT TTAGAAAGAA TTGATTAGC GATAGACCAA	120
GCTGGTAAGC ACTCTGACTA CACGAAATTG TTCAGATGTG ATGGATTAT GACAGTTGAT	180
CTTTGGAAGA GATTATTAAG TGATTATTTT AAAGGAAATC CATTAAATTCC AGAATATCTT	240
GGTTTAGCTC AAGATGATAT AGAAATAGAA CAGAAAGAGA CTACAAATGA AGATGTATCA	300
CCAACTGATA TTGAAGAGCC TATAGTAGAA AATGAATTAG CTGCATTAT TAGCCTTACA	360
CATAGCGATT TTCCTGATGA ATCTTATATT CAGCCATCGA CATAGCATTA CCTGATGGC	420
AACCTTACGA ATAATAGAAA CTGGGTGCGG GGCTATTGAT GAATTCATCC NCAGTAAATT	480
TGGATATNAC AAAATATAAC TCGATTGCA TTGGATGATG GAATACTAAA TCTGGCAAAA	540
GTAACTTTGG AGCTACTAGT AACCTCTCTT TTTGAGATGC AAAATTCTT TTTAGGGTTT	600
CTTATTCTCT ACTTACCGA TATTGGAGCA TAAAGGGAA	638

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACTGATGGAT GTCGCCGGAG GCGAGGGGCC TTATCTGATG CTCGGCTGCC TGTTCGTGAT	60
GTGCGCGGCG ATTGGGCTGT TTATCTCAA CACCGCCACG GCGGTGCTGA TGGCGCCTAT	120
TGCCTTAGCG GCGCGAAGT CAATGGGCGT CTCACCCCTAT CCTTTGCCA TGGTGGTGGC	180
GATGGCGGCT TCGCGGCGT TTATGACCCC GGTCTCCTCG CCGGTTAACCA CCCTGGTGC	240
TGGCCCTGGC AAGTACTCAT TTAGCGATTT TGTCAAAATA GGCGTG	286

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TCGGTCATAG CAGCCCCCTTC TTCTCAATTT CATCTGTAC TACCCCTGGTG TAGTATCTCA	60
TAGCCTTACA TTTTTATAGC CTCCTCCCTG GTCTGTCTTT TGATTTTCCT GCCTGTAATC	120
CATATCACAC ATAACGTCAA GTAAACATTT CTAAAGTGTG GTTATGCTCA TGTCACTCCT	180
GTGNCAAGAA ATAGTTTCCA TTACCGTCTT AATAAAATTC GGATTGTTTC TTTNCTATTN	240
TCACTCTTCA CCTATGACCG AA	262

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCGGTCATAG CAAAGCCAGT GGTTTGAGCT CTCTACTGTG TAAACTCCTA AACCAAGGCC	60
ATTTATGATA AATGGTGGCA GGATTTTAT TATAAACATG TACCCATGCA AATTCCTAT	120
AACTCTGAGA TATATTCTTC TACATTAAA CAATAAAAAT AATCTATTTT TAAAAGCCTA	180
ATTTGCGTAG TTAGGTAAGA GTGTTAATG AGAGGGTATA AGGTATAAAT CACCAGTCAA	240
CGTTTCTCTG CCTATGACCG A	261

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TACAACGAGG CGACGTCGGT AAAATCGGAC ATGAAGCCAC CGCTGGTCTT TTCGTCCGAG	60
CGATAGGCAGC CGGCCAGCCA GCGGAACGGT TGCCCGGATG GCGAAGCGAG CCGGAGTTCT	120
TCGGACTGAG TATGAATCTT GTTGTGAAAA TACTCGCCGC CTTCGTTCGA CGACGTCGCG	180
TCGAAATCTT CGANCTCCTT ACGATCGAAG TCTTCGTGGG CGACGATCGC GGTCAGTTCC	240
GCCCCACCGA AATCATGGTT GAGCCGGATG CTGNCCCCGA AGNCCTCGTT TGTN	294

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTGGTAAAGG GCATGGACGC AGACGCCCTGA CGTTGGCTG AAAATCTTTC ATTGATTCTGT	60
ATCAATGAAT AGGAAAATTC CCAAAGAGGG AATGTCCTGT TGCTGCCAG TTTTTNTGTT	120
GTTCTCATGG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CAACTAGTCG NCTTGCNANG ATCTTCAT	208

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

NCCNTTGAGC TGAGTGATTG AGATNTGTAAG TGTTGTAAG GGTGATTCAAG GCGGATTAGG	60
GTGGCGGGTC ACCCGGCAGT GGGTCTCCCG ACAGGCCAGC AGGATTGGG GCAGGTACGG	120
NGTGCGCATC GCTCGACTAT ATGCTATGGC AGGCCAGCCG TGGAAAGGNGG ATCAGGTACAC	180
GGCGCTGGAG CTTTCCACGG TCCATGNATT GNGATGGCTG TTCTAGGCAG CTGTTGCCAA	240
GCCTGATGGT ACGCTGGCTG GAGCATTGAT TTCTGGTGCC AAGGTGG	287

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTGGGTAAAG GGAGCAAGGA GAAGGCATGG AGAGGCTCAN GCTGGTCCTG GCCTACGACT	60
GGGCCAAGCT GTGCCGGGG ATGGTGGAGA ACTGAAGCGG GACCTCCTCG AGGTCTCCG	120
NCGTTACTTC NCCGTCCAGG AGGAGGGTCT TTCCGTGGTC TNGGAGGAGC GGGGGGAGAA	180
GATNCTCTC ATGGTCNACA TCCC	204

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGGATTGGTC AGGAGCGGGT AGAGTGGCAC CATTGAGGGG ATATTCAAAA ATATTATTTT	60
GTCCTAAATG ATAGTTGCTG AGTTTTCTT TGACCCATGA GTTATATTGG AGTTTATTTT	120
TTAACCTTCC AATCGCATGG ACATGTTAGA CTTATTTCT GTTAATGATT NCTATTTTA	180

TTAAATTGGA TTTGAGAAAT TGGTTNTTAT TATATCAATT TTTGGTATTT GTTGAGTTG	240
ACATTATAGC TTAGTATGTG ACCA	264

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTACAACGAG GGGAAACTCC GTCTCTACAA AAATTAAAAAA ATTAGCCAGG TGTGGTGGTG	60
TGCACCCGCA ATCCAGCTA CTTGGGAGGT TGAGACACAA GANTCACCTA NATGTGGGAG	120
GTCAAGGTTG CATGAGTCAT GATTGTGCCA CTGCACTCCA GCCTGGGTGA CAGACCGAGA	180
CCCTGCCTCA ANAGANAANG AATAGGAAGT TCAGAAATCN TGGNTGTGGN GCCCAGCAAT	240
CTGCATCTAT NCAACCCCTG CAGGCAANG TGATGCAGCC TANGTTCAAG AGCTGCTGTT	300
TCTGGAGGCA GCAGTTNGGG CTTCCATCCA GTATCACGGC CACACTCGCA CNAGCCATCT	360
GTCCTCCGTN TGTNAC	376

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTACAACGAG GGGAAACTCC GTCTCTACAA AAATTAAAAAA ATTAGCCAGG TGTGGTGGTG	60
TGCACCTGTA ATCCAGCTA CTTGGCGGGC TGAGACACAA GAACCACCTA AATGTGGGAG	120
GGTCAAGGTT GCATGAGTCAT TGATCGGCC ACTGCACTCC AGCCTGGGTG ACAGACTGAG	180
ACCCCTGCCTC AAAAGAAAAA GAATAGGAAG TTCAGAAACC CTGGGTGTGG NGCCCAGCAA	240
TCTGCATTTC AACAAATCCCT GCAGGCAATG CTGATGCAGC CTAAGTTCAA GAGCTGCTGT	300
TCTGGAGGCA GNAGTAAGGG CTTCCATCCA GCATCACGGN CAACACTGCA AAAGCACCTG	360
TCCTCGTTGG TA	372

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTCTGTCCAC ATCTACAAGT TTTATTTATT TTGTGGTTT TCAGGGTGAC TAAGTTTTC	60
CCTACATTGA AAAGAGAAGT TGCTAAAAGG TGCACAGGAA ATCATTTC TAAAGTGAATA	120
TGATAATATG GGTCCGTGCT TAATACAAC T GAGACATATT TGTCTCTGT TTTTTAGAG	180

TCACCTCTTA AAGTCCAATC CCACAATGGT GAAAAAAAATAGAAAGTAT TTGTTCTACC	240
TTTAAGGAGA CTGCAGGGAT TCTCCTTGAA AACGGAGTAT GGAATCAATC TAAATAAAT	300
ATGAAATTGG TTGGTCTTCT GGGATAAGAA ATTCCTTCACT CAGTGTGCTG AAATTCACCT	360
GACTTTTTT GGGAAAAAT AGTCGAAAT GTCAATTGG TCCATAAAAT ACATGTTACT	420
ATTAAAAGAT ATTTAAAGAC AAATTCTTCA AGAGCTCTAA GATTGGTGTG GACAGAA	477

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TCTNCAACCT CTTGANTGTC AAAAACCTTN TAGGCTATCT CTAAAAGCTG ACTGGTATT	60
ATTCCAGCAA AATCCCTCTA GTTTTTGAG TTTCCCTTTA CTATCTGGGG CTGCCTGAGC	120
CACAAATGCC AAATTAAGAG CATGGCTATT TTCCGGGGCT GACAGGTCAA AAGGGGTGTA	180
AATCCGATAA GCCTCCTGGA GGTGCTCTAA AAACACTCCT GGTGACTCAT CATGCCCTG	240
GACGACTTCA ATCGNCTTAG ACAAGTTAT AGGTTTCTGG GCAGCTCCCT GAATACCCAC	300
GAGGAGATAC CGGTGGAAAT CGTCAAAGT TCTCCCTCCA CTTGAGAAAT TTGGGTCCCA	360
ATTAGGTCCC AATTGGTCT CTAATCACTA TTCCCTCTAGC TTCCCTCCTCC GGNCTATTGG	420
TTGATGTGAG GTTGAAGA	438

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAGAGGGTAC CAGCCCCAAG CCTTGACAAC TTCCATAGGG TGTCAAGCCT GTGGGTGCAC	60
AGAAGTCAAA AATTGAGTTT TGGGATCCTC AGCCTAGATT TCAGAGGATA TAAAGAAACA	120
CCTAACACCT AGATATTCAAG ACAAAAGTTT ACTACAGGGA TGAAGCTTTC ACGGAAAACC	180
TCTACTAGGA AAGTACAGAA GAGAAATGTG GTTGGAGC CCCCAAACAG AATCCCTCT	240
AGAACACTGC CTAATGAAAC TGTGAGAAGA TGGCCACTGT CATCCAGACA CCAGAATGAT	300
AGACCCACCA AAAACTTATG CCATATTGCC TATAAAACCT ACAGACACTC AATGCCAGCC	360
CCATGAAAAA AAAACTGAGA AGAAGACTGT NCCCTACAAT GCCACCGGAG CAGAACTGCC	420
CCAGGCCATG GAAGCACAGC TCTTATATCA ATGTGACCTG GATGTTGAGA CATGGAATCC	480
NANGAAATCN TTTTAANACT TCCACGGTTN AATGACTGCC CTATTANATT CNGAACTTAN	540
ATCCNGGCT GTGACCTCTT TGCTTTGGCC ATTCCCCCTT TTTGGAATGG CTNTTTTTT	600
CCCATGCCTG TNCCCTCTTA	620

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTACAAACGAG GGGGTCAATG TCATAAATGT CACAATAAAA CAATCTCTTC TTTTTTTTTT	60
TTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT	100

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TAGTCTATGC GCCGGACAGA GCAGAATTAA ATTGGAAGTT GCCCTCCGGA CTTTCTACCC	60
ACACTCTTCC TGAAAAGAGA AAGAAAAGAG GCAGGAAAGA GGTAGGATT TCATTTCAA	120
GAGTCAGCTA ATTAGGAGAG CAGAGTTAG ACAGCAGTAG GCACCCATG ATACAAACCA	180
TGGACAAAGT CCCTGTTAG TAACTGCCAG ACATGATCCT GCTCAGGTTT TGAAATCTCT	240
CTGCCCATAA AAGATGGAGA GCAGGAGTGC CATCCACATC AACACGTGTC CAAGAAAGAG	300
TCTCAGGGAG ACAAGGGTAT CAAAAAACAA GATTCTTAAT GGGAAAGGAAA TCAAACACAAA	360
AAATTAGATT TTTCTCTACA TATATATAAT ATACAGATAT TTAACACATT ATTCCAGAGG	420
TGGCTCCAGT CCTTGGGGCT TGAGAGATGG TGAAAACATT TGTTCCACAT TAACTTCTGC	480
TCTCAAATTC TGAAGTATAT CAGAATGGGA CAGGCAATGT TTTGCTCCAC ACTGGGGCAC	540
AGACCCAAAT GGTTCTGTGC CCGAAGAAGA GAAGCCGAA AGACATGAAG GATGCTTAAG	600
GGGGGTTGGG AAAGCCAAAT TGGTANTATC TTTTCTCCT GCCTGTGTT CNGAAGTCTC	660
CNCTGAAGGA ATTCTTAAAA CCCTTTGTGA GGAAATGCC CCTTACCATG ACAANTGGTC	720
CCATTGCTT TAGGGNGATG GAAACACCAA GGGTTTGAT CC	762

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TAGTCTATGC GTGTATTAAC CTCCCCCTCCC TCAGTAACAA CCAAAGAGGC AGGAGCTGTT	60
ATTACCAACC CCATTTACA GATGCATCAA TAATGACAGA GAACTGAAGT GACTTGCGCA	120
CACAACCAGT AAATTGGCAG AGTCAGATTT GAATCCATGG AGTCTGGTCT GCACCTTCAA	180
TCACCGAATA CCCTTCTAA GAAACGTGTG CTGAATGAGT GCATGGATAA ATCAGTGTCT	240
ACTCAACATC TTTGCCTAGA TATCCCGCAT AGACTA	276

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TAGTAGTTGC CAAATATTTG AAAATTACC CAGAAAGTGT	TGAAAAC	60
AAACAAATAA AGCCAAAAGG TAAAATAAAA ATATCTTG	ACTCTCGTTA TTACCTATCC	120
ATAACTTTT CACCGTAAGC TCTCCTGCTT GTTAGTGTAG	TGTGGTTATA TTAAAC	180
TAGTTATTAT TTTTATTCA CTTTCCACT AGAAAGTCAT	TATTGATTAA GCACACATGT	240
TGATCTCATT TCATTTTTTC TTTTATAGG CAAAATTGA	TGCTATGCAA CAAAATACT	300
CAAGCCCATT ATCTTTTTTC CCCCCGAAAT CTGAAAATTG	CAGGGGACAG AGGGAAGTTA	360
TCCCATTAAA AAATTGTAAA TATGTTCACT TTATGTTAA	AAATGCACAA AACATAAGAA	420
AATTGTGTTT ACTTGAGCTG CTGATTGAA GCAGTTTAT	CTCAGGGGCA ACTACTA	477

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 631 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TAGTAGTTGC CAATTCAAGAT GATCAGAAAT GCTGCTTTCC	TCAGCATTGT CTTGTTAAC	60
CGCATGCCAT TTGAAACTTT GGCAGTGAGA AGCCAAAAGG	AAGAGGTGAA TGACATATAT	120
ATATATATAT ATTCAATGAA AGTAAAATGT ATATGCTCAT	ATACCTTCTA GTTATCAGAA	180
TGAGTTAAGC TTTATGCCAT TGGGCTGCTG CATATTTAA	TCAGAAGATA AAAGAAAATC	240
TGGGCATTT TAGAATGTGA TACATGTTT TTTAAAAC	TTGAAATATTA TTTCGATATT	300
TGTCTAAGAA CCGGAATGTT CTTAAAATTT ACTAAAACAG	TATTGTTGA GGAAGAGAAA	360
ACTGTACTGT TTGCCATTAT TACAGTCGTA CAAGTGCATG	TCAAGTCACC CACTCTCTCA	420
GGCATCAGTA TCCACCTCAT AGCTTACAC ATTTGACGG	GGAAATATTGC AGCATCCTCA	480
GGCCTGACAT CTGGGAAAGG CTCAGATCCA CCTACTGCTC	CTTGCTCGTT GATTGTTTT	540
AAAATATTGT GCCTGGTGTC ACTTTAAGC CACAGCCCTG	CCTAAAAGCC AGCAGAGAAC	600
AGAACCCGCA CCATTCTATA GGCAACTACTA	A	631

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 578 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TAGTAGTTGC CATCCCATAT TACAGAAGGC TCTGTATACA	TGACTTATTT GGAAGTGATC	60
TGTTTCTCT CCAAACCCAT TTATCGTAAT TTCACCAGTC	TTGGATCAAT CTTGGTTCC	120
ACTGATACCA TGAAACCTAC TTGGAGCAGA CATTGCACAG	TTTCTGTGG TAAAAC	180
AGGTTTATTT GCTAAGCTGT CATCTTATGC TTAGTATT	TTTTTACAG TGGGAATTG	240
CTGAGATTAC ATTTGTTAT TCATTAGATA CTTGGGATA	ACTTGACACT GTCTTCTTT	300
TTTCGTTTT AATTGCTATC ATCATGCTTT	TGAAACAAGA ACACATTAGT CCTCAAGTAT	360

TACATAAGCT TGCTTGTAC GCCTGGTGGT TTAAAGGACT ATCTTGGCC TCAGGTTCAC	420
AAGAATGGC AAAGTGTTC CTTATGTTCT GTAGTTCTCA ATAAAAGATT GCCAGGGGCC	480
GGGTACTGTG GCTCGCACTG TAATCCCAGC ACTTTGGGAA GCTGAGGCTG CGGGATCATG	540
TTAGGGCAGG TGTCGAAAC CAGCCTGGGC AACTACTA	578

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TAGTAGTTGC CTGTAATCCC AGCAACTCAG GAGGCTGGGG CAGGAGAAC AGTTGAACCT	60
GGGAGGCAGA AGTTGTAATT AGCAAAGATC GCACCATTGC ACTTCAGCCT GGGCAACAAG	120
AGTGAGATT CATCTAAAAA ACAAAAAAAA GAAAAAGAAA AGAAAAGGAA AAAACGTATA	180
AAACCCAGCCA AAACAAAATG ATCATTCTTT TAATAAGCAA GACTAATTAA ATGTGTTTAT	240
TTAATCAAAG CAGTTGAATC TTCTGAGTTA TTGGTGAAAA TACCCATGTA GTTAATTAG	300
GGTTCTTACT TGGGTGAACG TTTGATGTT ACAGGTTATA AAATGGTTAA CAAGGAAAAT	360
GATGCATAAA GAATCTTATA AACTACTAAA AATAAAATAA ATATAAAATGG ATAGGTGCTA	420
TGGATGGAGT TTTTGTGTAA TTTAAAATCT TGAAGTCATT TTGGATGCTC ATTGGTTGTC	480
TGGTAATTTC CATTAGGAAA AGGTTATGAT ATGGGGAAAC TGTTCTGGA AATTGCGGAA	540
TGTTCTCAT CTGAAAATG CTAGTATCTC AGGGCAACTA CTA	583

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATCTACTAG TCATNTGGAT TCTATCCATG GCAGCTAACG CTTTCTGAAT GGATTCTACT	60
GCTTTCTTGT TCTTTAATCC AGACCCTTAT ATATGTTTAT GTTCACAGGC AGGGCAATGT	120
TTAGTGAAAA CAATTCTAAA TTTTTTATTT TGCACTTCA TGCTAATTTC CGTCACACTC	180
CAGCAGGCTT CCTGGGAGAA TAAGGAGAAA TACAGCTAAA GACATTGTCC CTGCTTACTT	240
ACAGCCTAAT GGTATGCAA ACCACTTCAA TAAAGTAACA GGAAAAGTAC TAACCAGGTA	300
GAATGGACCA AACTGATAT AGAAAATCA GAGGAAGAGA GGAACAAATA TTTACTGAGT	360
CCTAGAATGT ACAAGGCTTT TTAATTACAT ATTTTATGTA AGGCCTGCAA AAAACAGGTG	420
AGTAATCAAC ATTTGTCCCA TTTTACATAT AAGGAAACTG AAGCTTAAAT TGAATAATT	480
AATGCATAGA TTTTATAGTT AGACCATGTT CAGGTCCCTA TGTTATACTT ACTAGCTGTA	540
TGAATATGAG AAAATAATT TGTTATTTC TTGGCATOAG TATTTCATC TGCAAAATAA	600
AGCTAAAGTT ATTTAGCAA CAGTCAGCAT AGTGCCTGAT ACATAGTAGG TGCTCCAAAC	660
ATGATTACNC TANTATTNGG TATTAAAAA ATCCAATATA GGCNTGGATA AAACCG	716

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTCTGTCCAC ATATCATCCC ACTTTAATTG TTAATCAGCA AAACCTTCAA TGAAAAATCA	60
TCCATTAA CCAGGATCAC ACCAGGAAAC TGAAGGTGTA TTTTTTTTAA CCTTAAAAAA	120
AAAAAAAAAA ACCAACAAA CCAAAACAGA TTAACAGCAA AGAGTTCTAA AAAATTACAA	180
TTTCTCTTAC AACTGTCATT CAGAGAACAA TAGTTCTTAA GTCGTGTTAA TCTTGGCATT	240
AACAGAGAAA CTTGATGAAN AGTTGTACTT GGAATATTGT GGATTTTTT TTTTGTCTAA	300
TCTCCCCCTA TTGTTTGC C AACAGTAATT TAAGTTGTG TGGAACATCC CCGTAGTTGA	360
AGTGTAAACA ATGTATAGGA AGGAATATAT GATAAGATGA TGCATCACAT ATGCATTACA	420
TGTAGGGACC TTCACAACTT CATGCACTCA GAAAACATGC TTGAAGAGGA GGAGAGGACG	480
GCCCAGGGTC ACCATCCAGG TGCCTGAGG ACAGAGAATG CAGAAGTGGC ACTGTTGAAA	540
TTTAGAAGAC CATGTGTGAA TGGTTTCAGG CCTGGATGT TTGCCACCAA GAAGTGCCTC	600
CGAGAAATTCTT CTTTCCCATT TGGAAATACAG GGTGGCTTGA TGGGTACGGT GGGTGACCCA	660
ACGAAGAAAA TGAAATTCTG CCCTTTCC	688

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TAGTAGTTGC CGCNNACCTA AAANTTGGAA AGCATGATGT CTAGGAAACA TANTAAAATA	60
GGGTATGCCT ATGTGCTACA GAGAGATGTT AGCATTAA GTGCATANTT TTATGTATTT	120
TGACAAATGC ATATNCCTCT ATAATCCACA ACTGATTACG AAGCTATTAC AATTAAAAG	180
TTTGGCCGGG CGTGGTGGGC GGTGGCTGAC GCCTGTAATC CCAGCACTTT GGGAGGCCGA	240
GGCACGCCGA TCACGAGGTC GGGAGTTCAA GACCACCTG GCTAACACGG TGAAAGTCCA	300
TCTCTACTAA AAATACGAAA AAATTACCCC GGCGTGGTGG CGGGCGCCTG TAGTCCCAGC	360
TACTCCGGAG GCTGAGGCAG GAGAATGGCG TGAACCCAGG ACACGGAGCT TGCAGTGTGC	420
CAACATCACG TCACTGCCCT CCAGCTGGG GGACAGGAAC AAGANTCCCG TCCTCANAAA	480
AGAAAATAC TACTNATANT TTCNACTTTA TTTTAANTTA CACAGAACTN CCTCTTGGTA	540
CCCCCTTACC ATTCACTCTCA CCCACCTCCT ATAGGGCACN NCTAA	585

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TCTGTCCACA CCAATCTTAG AAGCTCTGAA AAGAATTGT CTTTAAATAT CTTTTAATAG	60
TAACATGTAT TTTATGGACC AAATTGACAT TTTGACTGT TTTTCCAAA AAAGTCAGGT	120

GAATTCAGC ACAGTGAGTT GGGAAATTCT TATCCCAGAA GACCAACCAA TTTCATATTT	180
ATTTAAGATT GATTCCATAC TCCGTTTCA AGGAGAATCC CTGCAGTCTC CTTAAAGGTA	240
GAACAAATAC TTCTATTT TTTTCACCA TTGTGGGATT GGACTTAAG AGGTGACTCT	300
AAAAAAACAG AGAACAAATA TGTCTCAGTT GTATTAAGCA CGGACCCATA TTATCATATT	360
CACTAAAAAA AATGATTTCC TGTGCACCTT TTGGCAACTT CTCTTTCAA TGTAGGGAAA	420
AACTTAGTCA CCCTGAAAAC CCACAAAATA AATAAAACTT GTAGATGTGG ACAGA	475

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TAAGAGGGTA CATCGGGTAA GAACGTAGGC ACATCTAGAG CTTAGAGAAG TCTGGGGTAG	60
GAAAAAAATC TAAGTATTAA TAAGGGTATA GGTAAACATT AAAAGTAGGG CTAGCTGACA	120
TTATTTAGAA AGAACACATA CGGAGAGATA AGGGCAAAGG ACTAAGACCA GAGGAACACT	180
AATATTAGT GATCACTTC ATTCTGGTA AAAATAGTAA CTTTTAAGTT AGCTTCAAGG	240
AAGATTTTG GCCATGATTA GTGTCAAAA GTTAGTTCTC TTGGGTTTAT ATTACTAATT	300
TTGTTTAAG ATCCTTGTAA GTGTTTAAT AAAGTCATGT TATATCAAAC GCTCTAAAAC	360
ATTGTAGCAT GTTAAATGTC ACAATATACT TACCAATTGT TGTATATGGC TGTACCCCTCT	420
CTA	423

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCTCCTAGGC TAATGTGTGT GTTTCTGTAA AAGTAAAAAG TTAAAAATTAA TAAAAATAGA	60
AAAAAGCTTA TAGAATAAGA ATATGAAGAA AGAAAATATT TTTGTACATT TGCACAATGA	120
GTTTATGTAAAGT TAAGCTAAAGT GTTATTACAA AAGAGCCAA AAGGTTTAA AAATTTAAAC	180
GTTTGTAAAG TTACAGTACC CTTATGTAA TTTATAATTG AAGAAAAGAAA AACTTTTTT	240
TATAAAATGTA GTGTAGCCTA AGCATAACAGT ATTTATAAAAG TCTGGCAGTG TTCAATAATG	300
TCCTAGGCCT TCACATTACAC TCACTGACTC ACCCAGAGCA ACTTCCAGTC CTGTAAGCTC	360
CATTCGTGGT AAGTGCCTA TACAGGTGCA CCATTTATT TACAGTATT TTACTGTACC	420
TTCTCTATGT TTCCATATGT TTCGATATAC AAATACCACT GGTTACTATN GCCCNACAGG	480
TAATTCCAGT AACACGGCCT GTATACGTCT GGTANCCCTA GNGAAGA	527

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TCTTCAACCT CGTAGGACAA CTCTCATATG CCTGGCACT ATTTTAGGT TACTACCTTG	60
GCTGCCCTTC TTTAAGAAAA AAAAAGAAG AAAAAGAAC TTTCCACAA GTTCTCTTC	120
CTCTAGTTGG AAAATTAGAG AAATCATGTT TTTAATTG TGTTATTCA GATCACAAAT	180
TCAAACACTT GTAAACATTA AGCTTCTGTT CAATCCCCTG GGAAGAGGAT TCATTCTGAT	240
ATTTACGGTT CAAAAGAAGT TGTAATATTG TGCTTGAAC ACAGAGAACC AGTTATTAAC	300
TTCCTACTAC TATTATATAA TAAATAATAA C	331

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGCTTAGTAG TTGCCAGGCA AAATARCGTT GATTCTCCTC AGGAGCCACC CCCAACACCC	60
CTGTTGCTT CTAGACCTAT ACCTAGACTA AAGTCCCAGC AGACCCCTAG AGGTGAGGTT	120
CAGAGTGACC CTTGAGGAGA TGTGCTACAC TAGAAAAGAA CTGCTTGACT TTTCTAATTT	180
ATATAAGCAG AAATCTGGAG AAGAGTCATA GGAATGGATA TTAAGGGTGT GAGATAATGG	240
CGGAAGGAAT ATAGAGTTGG ATCAGGCTGG ACTTATTGAT TTGAACCCAC TAAGTAGAGA	300
TTCTGTTTT GATGTTGCAG CTCAGGGAGT TAAAAAAAGGT TTTAATGGTT CTAATAGTTT	360
ATTGCTTGG TTAGCTGAAA TATGGATAAA AGATGGCCA CTGTGAGCAA GCTGGAAATG	420
CCTGATCTCT CTCAGTTAA TGTAGAGGAA GGGATCCAAA AGTTTAGGGA GANTGGATG	480
CTGGRAKTTGG ATTGGTCACT TTGRGACCTA CCCWTCCAG CTGGGAGGGT CCAGAAGATA	540
CACCCTTGAC CAACGCTTTG CGAAATGGAT TTGTGATGGC GGCAACTACT AA	592

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGCTTAGTAG TTGCCATTGC GAGTGCTTGC TCAACGAGCG TTGAACATGG CGGATTGTCT	60
AGATTCAACG GATTTGAGTT TTACCAAGCAA AGCGAACCAA GCGCGGCCCA GAGAATTATG	120
GGTTGGTTGG CTTTGAAGGAA ATGGAAATCC TGTAGGCCTA GTCAGAAAAG CCTTCTTGCA	180
GAACAGTTGG TTCTCGGGCG AACGCTCATC AAGATGCCA TTGGAAAGGC TAGCGTGTAT	240
TTGGGAGAGC CTGATAGCGT GTCTTCTGAT GATGTTGAGT CTTGGACAGT GACAAAAGAT	300
ATGCAAAGCA AGTCCGAAC AGACGTCAAG CTTCTGTGAGC AAATTATTGT AGACTCCTAC	360
TTATACTGTG AGGAATGATA GCCAAGGGTG GGGACTTTAA GACTAAGGTG GTTTGTACTT	420
GCGCCGATGA TCCCAGGCAG AAAGAMCTGA TCGCTAGTT TATACGGGCA ACTACTAAGC	480
CGAATTCCAG CACACTGGCG GCCGTTACTA ATTGGATCCG ANCTCGGTAC CAGCTTGATG	540
CATASCTTGA GTTWTCTATA NTGTCNC	567

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 908 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GAGCGAAAGA	CCGAGGGCAG	NGNNNTANGNG	CGANGAAGCG	GAGAGGGCCA	AAAAGCAACC	60
GCTTTCCCCG	GGGGGTGCCG	ATTCAATTAAAG	GCAGGGTGGAG	GACAGGTTTC	CCGATGGAAG	120
CGGGCAGGGG	CGCAAGCAAT	TAATGTGAGT	AGGCCATTC	TTAGCACCCG	GGCTTAACAT	180
TTAAGCTTCG	GGTTGGTATG	TGGTGGGAAT	TGTGAGCGGA	TAACAATTTC	ACACAGGAAA	240
CAGCTATGAC	CATGATTACG	CCAAGCTATT	TAGGTGACAT	TATAGAATAA	CTCAAGTTAT	300
GCATCAAGCT	TGGTACCGAG	TTCGGATCCA	CTAGTAACGG	CCGCCAGTGT	GTGGAATTCG	360
GCTTAGTGT	TGCCGACCAT	GGAGTGCTAC	CTAGGCTAGA	ATACCTGAGY	TCCTCCCTAG	420
CCTCACTCAC	ATTAAATTGT	ATCTTTCTA	CATTAGATGT	CCTCAGCGCC	TTATTTCTGC	480
TGGACWATCG	ATAAAATTAAAT	CCTGATAGGA	TGATAGCAGC	AGATTAATTA	CTGAGAGTAT	540
GTAAATGTGT	CATCCCTCCT	ATATAACGTA	TTTGCATTT	AATGGAGCAA	TTCTGGAGAT	600
AATCCCTGAA	GGCAAAGGAA	TGAATCTTGA	GGGTGAGAAA	GCCAGAAATCA	GTGTCCAGCT	660
GCAGTTGTGG	GAGAAGGTGA	TATTATGTAT	GTCTCAGAAG	TGACACCATA	TGGGCAACTA	720
CTAAGCCCGA	ATTCCAGCAC	ACTGGCGGGC	GTTACTAATG	GATCCGAGCT	CGGTACCAAG	780
CTTGATGCAT	AGCTTGAGTA	TCTATAGTGT	CACTAAATAG	CCTGGCGTTA	TCATGGTCAT	840
AGCTGTTCC	TGTGTGAAAT	TGTTATCCGC	TCCCAATTCC	CCCCACCATA	CGAGCCGGAA	900
	CATAAAAGT					908

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TGCCAACAAAG	GAAAGTTTTA	AATTCCCCCT	TGAGGATTCT	TGGTGATCAT	CAAATTCACT	60
GGTTTTTAAG	GTTGTTTCT	GTCAAATAAC	TCTAACTTTA	AGCCAAACAG	TATATGGAAG	120
CACAGATAKA	ATATTACACA	GATAAAAGAG	GAGTTGATCT	AAAGTARAGA	TAGTTGGGGG	180
CTTTAATTTC	TGGAACCTAG	GTCTCCCCAT	CTTCTTCTGT	GCTGAGGAAC	TTCTTGGAAAG	240
CGGGGATTCT	AAAGTTCTTT	GGAAAGACAGT	TTGAAAACCA	CCATGTTGTT	CTCAGTACCT	300
TTATTTTAA	AAAGTAGGTG	AACATTTGA	GAGAGAAAAG	GGCTTGGTTG	AGATGAAGTC	360
CCCCCCCCCC	CTTTTTTTTT	TTTTAGCTGA	AATAGATACC	CTATGTTNAA	RGAARGGATT	420
ATTATTTACC	ATGCCAYTAR	SCACATGCTC	TTTGATGGGC	NYCTCCSTAC	CCTCCTTAAG	480

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAGAGGGTAC CGAGTGGAAAT TTCCGCTTCA CTAGTCTGGT GTGGCTAGTC GGTTTCGTGG	60
TGGCCAACAT TACGAACCTTC CAACTCAACC GTTCTGGAC GTCAAGCGG GAGTACCGGC	120
GAGGATGGTG GCGTGAATTTC TGGCCTTTCT TTGCCGTGGG ATCGGTAGCC GCCATCATCG	180
GTATGTTTAT CAAGATCTTC TTTACTAACCG ACACCTCTCC GATTTACCTG CCCGAGCCGT	240
GGTTAACGA GGGGAGGGGG ATCCAGTCAC GCGAGTACTG GTCCCAGATC TTCGCCATCG	300
TCGTGACAAT GCCTATCAAC TTGCGTGTCA ATAAGTTGTG GACCTTCCGA ACGGTGAAGC	360
ACTCCGAAAA CGTCCGGTGG CTGCTGTGCG GTGACTCCCA AAATCTTGAT AACAAACAAGG	420
TAACCGAATC GCGCTAAGGA ACCCCGGCAT CTCGGGTACT CTGCATATGC GTACCCCTTA	480
AGCCGAATTC CAGCACACTG GCGGCCGTAA CTAATTGGAT CCGAACTCCG TAACCAAGCC	540
TGATGCGTAA CTTGAGTTAT TCTATAGTGT CCCTAAAATA ACCTGGCGTT A	591

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AAGAGGGTAC CTGCCTTGAA ATTTAAATGT CTAAGGAAAR TGGGAGATGA TTAAGAGTTG	60
GTGTGGCYTA GTCACACCAA AATGTATTTA TTACATCCTG CTCCTTTCTA GTTGACAGGA	120
AAGAAAGCTG CTGTGGGGAA AGGAGGGATA AATACTGAAG GGATTTACTA AACAAATGTC	180
CATCACAGAG TTTTCCTTT TTTTTTTTG AGACAGAGTC TTGCTCTGTC ACCCAGGCTG	240
GAATGAAGWG GTATGATCTC AGTTGAATGC AACCTCTACC TCCTAGGTTC AAGCGATTCT	300
CATGCCTCAG CCTCCTGAGC AGCTGGGACT ATAGGCCAT GCTACCATGC CAGGCTAATT	360
TTTATATTTT TATTAGAGAC GGGGTGTTGC CATGTTGGCC AGGCAGGTCT CGAACTCCTG	420
GGCCTCAGAT GATCTGCCCT ACCGTACCCCT CTTA	454

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAGAGGGTAC CAAAAAAAAG AAAAAGGAAA AAAAGAAAAA CAACTTGTAT AAGGCTTTCT	60
GCTGCATACA GCTTTTTTTT TTTAAATAAA TGGTGCCAAC AAATGTTTT GCATTCACAC	120
CAATTGCTGG TTTTGAAATC GTACTCTTCA AAGGTATTG TGCAAGATCAA TCCAATAGTG	180
ATGCCCGTA GGTGTTGTGG ACTGCCACG TTGCTCACCT TCTCATGTAG GAGCCATTGA	240
GAGACTGTGTT GGACATGCCT GTGTTCATGT AGCCGTGATG TCCGGGGGCC GTGTACATCA	300
TGTTACCGTG GGGTGGGGTC TGCATTGGCT GCTGGGCATA TGGCTGGGTG CCCATCATGC	360
CCATCTGCAT CTGCATAGGG TATTGGGGCG TTGATCCAT ATAGCCATGA TTGCTGTGGT	420
AGCCACTGTT CATCATTGGC TGGGACATGC TGTTACCCCTC TTA	463

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTTCAACCTC CCAAAGTGCT GGGATTACAG GACTGAGCCA CCACGCTCAG CCTAACGCCTC	60
TTTTCACTA CCCTCTAACG GATCTACCAAC AGTGATGAGG GGCTAAAGAG CAGTGCAATT	120
TGATTACAAT AATGGAACCTT AGATTATTAA ATTAACAATT TTTCTTAGC ATGTTGGTTC	180
CATAATTATT AAGAGTATGG ACTTACTTAG AAATGAGCTT TCATTTTAAG AATTCATCT	240
TTGACCTTCT CTATTAGTCT GAGCAGTATG ACACATACG TATTTTATTAACTAACCTA	300
CCTTGAGCTA TTACTTTTA AAAGGCTATA TACATGAATG TGTATTGTCA ACTGTAAGC	360
CCCACAGTAT TTAATTATAT CATGATGTCT TTGAGGTTG	399

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTTCAACCTC AATCAACCTT GGTAATTGAT AAAATCATCA CTTAACCTTC TGATATAATG	60
GCAATAATTAA TCTGAGAAAA AAAAGTGGTG AAAGATTAAA CTTGCATTTC TCTCAGAAC	120
TTGAAGGATA TTTGAATAAT TCAAAAGCGG AATCAGTAGT ATCAGCCGAA GAAACTCACT	180
TAGCTAGAAC GTTGGACCCA TGGATCTAAG TCCCTGCCCT TCCACTAACCC AGCTGATTGG	240
TTTTGTGTAA ACCTCCTACA CGCTTGGGCT TGGTCGCCCT ATTGTCAAA GTAAAGGCTG	300
AAATAGGAAG ATAATGAACC GTGTCTTTT GGTCTCTTT CCATCCATTA CTCTGATT	360
ACAAAGAGGC CTGTATTCCC CTGGTGAGGT TG	392

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TTCGGGTGAT GCCTCCTCAG GCTACAGTGA AGACTGGATT ACAGAAAGGT GCCAGCGAGA	60
TTTCAGATTC CTGTAAACCT CTAAAGAAAA GGAGTCGCGC CTCAACTGAT GTAGAAATGA	120
CTAGTTCAAGC ATACNGAGAC ACNTCTGACT CCGATTCTAG AGGACTGAGT GACCTGCAN	179

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTCGGGTGAT GCCTCCTAG GCTACATCAT NATAGAAGCA AAGTAGAANA ATCNNGTTG
TGCATTTCC CACANACAAA ATTCAAATGA NTGGAAGAAA TTGGGANAGT AT

60
112

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TGAGCTTCCG CTTCTGACAA CTCAAATAGAT AATCAAAGGA CAACTTTAAC AGGGATTAC
AAAGGAGTAT ATCCAAATGC CAATAAACAT ATAAAAAGGA ATTCAAGCTTC ATCATCATCA
GAAGWATGCA AATTAAAACC ATAATGAGAA ACCACTATGT CCCACTAGAA TAGATAAAAT
CTTAAAAGAC TGGTAAAACC AAGTGTGTT AAGGCAAGAG GAGCA

60
120
180
225

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCTCCTCTTG CCTTACCAAC ACATTCTCAA AAACCTGTTA GAGTCCTAAC CATTCTCCTG
TTAGTATTGG GATTTTACCC CTGTCCTATA AAGATGTTAT GTACCAAAAA TGAAGTGGAG
GGCCATACCC TGAGGGAGGG GAGGGATCTC TAGTGTGTC AGAAGCGGAA GCTCA

60
120
175

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

AGCCATTAC CACCCATGGA TGAATGGATT TTGTAATTCT AGCTGTTGTA TTTTGTGAAT

60

TTGTTAATTT TGTGTTTTCTGTGAAACA CATAACATTGG ATATGGGAGG TAAAGGAGTG	120
TCCCAGTTGC TCCTGGTCAC TCCCTTTATA GCCATTACTG TCTTGTTCCT TGTAACTCAG	180
GTAGGTTTT GGTCTCTCTT GCTCCACTGC AAAAAAAA AAA	223

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GTTCGAAGGT GAAACGTGAG GTAGCGGATC TCACAACTGG GGAACGTCA AAGACGAATT	60
AACTGACTTG GATCAATCAA ATGTGACTGA GGAAACACCT GAAGGTGAAG AACATCATCC	120
AGTGGCAGAC ACTGAAAATA AGGAGAATGA AGTTGAAGAG GTAAAAGAGG AGGGTCCAAA	180
AGAGATGACT TTGGATGGGT GGTAAATGGC T	211

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCTCCTCTTG CCTTACCAAC TTTGCACCCA TCATCAACCA TGTGCCAGG TTTGCAGCCC	60
AGGCTGCACA TCAGGGGACT GCCTCGAAAT ACTTCATGCT GTGCTGCTG ACTGATGGTG	120
CTGTGACGGA TGTGGAAGCC ACACGTGAGG CTGTGGTGGC TGCCCTGAAC CTGCCCATGT	180
CAGTGATCAT TATGGGTGGT AAATGGCT	208

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

AGCCATTAC CACCCATACT AAATTCTAGT TCAAACCTCCA ACTTCTTCCA TAAAACATCT	60
AACCACTGAC ACCAGTTGGC AATAGCTTCT TCCTTCTTAA ACCTCTTAGA GTATTTATGG	120
TCAATGCCAC ACATTTCTGC AACTGAATAA AGTTGGTAAG GCAAGAGGAG C	171

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGGGTGATGC CTCCTCAGGC TTTGGTGTGT CCACTCNACT CACTGGCCTC TTCTCCAGCA	60
ACTGGTGAAN ATGTCCTCAN GAAAANCNCC ACACGCNGCT CAGGGTGGGG TGGGAANCAT	120
CANAATCATC NGGC	134

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AGAGGGTACA TATGCAACAG TATATAAAGG AAGAAGTGCCTGAGAGGAA CTTCATCAAG	60
GCCATTTAAT CAATAAGTGA TAGAGTCAAG GCTCAACCCA GGTGTGACGG ATTCCAGGTC	120
CCAAGCTCCT TACTGGTACC CTCTT	145

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGCACTGAGA GGAATTCAAA GGGTTATGC CAAAGAACAA ACCAGTCCTC TGCAGCCTAA	60
CTCATTGTT TTTGGGCTGC GAAGCCATGT AGAGGGCGAT CAGGCAGTAG ATGGTCCCTC	120
CCACAGTCAG CGCCATGGTG GTCCGGTAAA GCATTTGGTC AGGCAGGCCT CGTTTCAGGT	180
AGACGGGCAC ACATCAGCTT TCTGGAAAAA CTTTTGTAGC TCTGGAGCTT TGTTTTCCC	240
AGCATAATCA TACACTGTGG AATCGGAGGT CAGTTAGTT GGTAAGGCAA GAGGAGC	297

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCAC TGAGAG GAACTTCCAA TACTATGTTG AATAGGAGTG GTGAGAGAGG GCATCCTTGT	60
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CTTGTGCCGG TTTCAAAAGG GAATGCTTCC AGCTTTGCC CATTCAAGTAT AATATTAAG	120
AATGTTTAC CATTCTGT CTTGCCTGTT TTTCTGTGTT TTTGTTGGTC TCTTCATTCT	180
CCATTTTAG GCCTTACAT GTTAGGAATA TATTCTTT AATGATACTT CACCTTGTT	240
ATCTTTGTG AGACTCTACT CATAGTGTGA TAAGCACTGG GTTGGTAAGG CAAGAGGAGC	300

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 203 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GCTCCTCTTG CCTTACCAAC TCACCCAGTA TGTCAGCAAT TTTATCRGCT TTACCTACGA	60
AACAGCCTGT ATCCAAACAC TTAACACACT CACCTGAAAA GTTCAGGCAA CAATGCCCTT	120
CTCATGGTC TCTCTGCTCC AGTTCTGAAC CTTTCTCTTT TCCTAGAACCA TGCATTARG	180
TCGATAGAAC TTCCTCTCAG TGC	203

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TACGGGGACC CCTGCATTGA GAAAGCGAGA CTCACTCTGA AGCTGAAATG CTGTTGCCCT	60
TGCAGTGCTG GTAGCAGGAG TTCTGTGCTT TGTGGGCTAA GGCTCCTGGA TGACCCCTGA	120
CATGGAGAAC GCAGAGTTGT GTGCCCTTC TCATGGCCTC GTCAAGGCAT CATGGACTGC	180
CACACACAAA ATGCCGTTT TATTAACGAC ATGAAATTGA AGGAGAGAAC ACAATTCACT	240
GATGTGGCTC GTAACCATGG ATATGGTCAC ATACAGAGGT GTGATTATGT AAAGGTTAAT	300
TCCACCCACC TCATGTGGAA ACTAGCCTCA ATGCAGGGGT CCCA	344

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCACTGAGAG GAACTTCGTA GGGAGGTTGA ACTGGCTGCT GAGGAGGGGG AACAAACAGGG	60
TAACCAGACT GATAGCCATT GGATGGATAA TATGGTGGTT GAGGAGGGAC ACTACTTATA	120
GCAGAGGGTT GTGTATAGCC TGAGGAGGCA TCACCCG	157

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCACTGAGAG GAACTTCTAG AAAGTAAAAG TCTAGACATA AAATAAAAATA AAAATTAAA ACTCAGGAGA GACAGCCCAG CACGGTGGCT CACGCCTGTA ATCCCAGAAC TTTGGGAGCC TGAGGAGGCA TCACCCG	60 120 137
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(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CGGGTGATGC CTCCTCAGGC TGTATTTGA AGACTATCGA CTGGACTTCT TATCAACTGA AGAATCCGTT AAAAATACCA GTTGTATTAT TTCTACCTGT CAAAATCCAT TTCAAATGTT GAAGTTCTC TCAGTGC	60 120 137
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(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AGCATGTTGA GCCCAGACAC GCAATCTGAA TGAGTGTGCA CCTCAAGTAA ATGTCTACAC GCTGCCTGGT CTGACATGGC ACACCACNC GTGGAGGGCA CASCTCTGCT CNGCCTACWA CGAGGGCANT CTCATWGACA GGTTCCACCC ACCAAACTGC AAGAGGCTCA NNAAGTACTR CCAGGGTMYA SGGACMASGG TGGGAYTYCA YCACWCATCT	60 120 180 220
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(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CGTTAGGGTC TCTATCCACT GCTAAACCAT ACACCTGGGT AAACAGGGAC CATTAAACAT	60
TCCCANCTAA ATATGCCAAG TGACTTCACA TGTTTATCTT AAAGATGTCC AAAACGCAAC	120
TGATTTCTC CCCTAAACCT GTGATGGTGG GATGATTAAN CCTGAGTGTT CTACAGCAAG	180
TTAAGTCAA GGTGCTAAAT GAANGTGACC TGAGATACAG CATCTACAAG GCAGTACCTC	240
TCAACNCAGG GCAACTTGC TTCTCANAGG GCATTTAGCA GTGTCTGAAG TAATTCTGT	300
ATTACAACTC ACGGGGCGGG GGGTGAATAT CTANTGGANA GNAGACCCTA ACG	353

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GCACTGAGAG GAACTTCAA TACYATKATC AGAGTGAACA RGCARCCYAC AGAACAGGAG	60
AAAATGTTYG CAATCTCTCC ATCTGACAAA AGGCTAATAT CCAGAWTCTA AWAGGAACTT	120
AAACAAATTT ATGAGAAAAG AACARACAAC CTCAWCAAAA AGTGGGTGAA GGAWATGCTS	180
AAARGAAGAC ATYTATTTCAG CCAGTAAACA YATGAAAAAA AGGCTCATSA TCACTGAWCA	240
TTAGAGAAAT GCAAATCAA ACCACAATGA GATACCATCT YAYRCCAGTT AGAAYGGTGA	300
TCATTAAR STCAGGAAAC AACAGATGCT GGACAAGGTG TCA	343

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCACTGAGAG GAACTTCAGA GAGAGAGAGA GAGTTCCACC CTGTACTTGG GGAGAGAAC	60
AGAAGGGTGAG AAAGTCTTG GTTCTGAAGC AGCTTCTAAG ATCTTTTCAT TTGCTTCATT	120
TCAAAGTTCC CATGCTGCCA AAGTGCATC CTTGGGTA CTGTTTCTG AGCTCCAGTG	180
ATAACTCATT TATACAAGGG AGATACCCAG AAAAAAAGTG AGCAAATCTT AAAAAGGTGG	240
CTTGAGTTCA GCCTTAAATA CCATCTTGAA ATGACACAGA GAAAGAANGA TGTTGGTGG	300
GAGTGGATAG AGACCCTAAC G	321

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GCACGTGAGAG GAACTTCAGA GAGAGAGAGA GAGTTCCACC CTGTACTTGG GGAGAGAAC	60
AGAAGGTGAG AAAGTCTTG GTTCTGAAGC AGCTTCTAAG ATCTTTTCAT TTGCTTCATT	120
TCAAAGTCC CATGCTGCCA AAGTGCCATC CTTGGGGTA CTGTTTCTG AGCTCCAGTG	180
ATAACTCATT TATACAAGGG AGATACCCAG AAAAAAAAGTG AGCAAATCTT AAAAAGGTGG	240
CTTGAGTTCA GYCTTAAATA CCATCTTGAA ATGAMACAGA GAAAGAAGGA TGTTGGTGG	300
GAGTGGATAG AGACCCTAAC G	321

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GCACGTGAGAG GAACTTCCAC ATGCACTGAG AAATGCATGT TCACAAGGAC TGAAGTCTGG	60
AACTCAGTTT CTCAGTTCCA ATCCTGATT AGGTGTTAC CAGCTACACA ACCTTAAGCA	120
AGTCAGATAA CCTTAGCTTC CTCATATGCA AAATGAGAAT GAAAAGTACT CATCGCTGAA	180
TTGTTTGAG GATTAGAAAA ACATCTGGCA TGCAGTAGAA ATTCAATTAG TATTCAATT	240
CATTCTTCTA AATTAAACAA ATAGGATTAG TAGTGGTGGA ACTTCAGACA CCAGAAATGG	300
GAGTGGATAG AGACCCT	317

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CGTTAGGGTC TCTATCCACT CCCACTACTG ATCAAACCTCT ATTATTTAA TTATTTTAT	60
CATACTTTAA GTTCTGGGAT ACACGTGCAG CATGCGCAGG TTTGTTGCAT AGGTATACAC	120
TTGCCATGGT GGTTTGCTGC ACCCATCAGT CCATCATCTA CATTAGGTAT TTCTCCTAAT	180
GCTATCCCTC CCCTAGCCCC TTACACCCCC AACAGGCTCT AGTGTGTGAA GTTCCTCTCA	240
GTC	244

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CGTTAGGGTC TCTATCCACT GAAATCTGAA GCACAGGAGG AAGAGAAGCA GTYCTAGTGA	60
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GATGGCAAGT TCWTTTACCA CACTTTAA CATTYYGTTT AGTTTAACC TTTATTATG	120
GATAATAAAG GTTAATATTA ATAATGATT ATTGAAAGGC ATTCCCRAAT TTGCATAATT	180
CTCCTTTGG AGATACCCCTT TTATCTCCAG TGCAAGTCTG GATCAAAGTG ATASAMAGAA	240
GTTCCTCTCA GTGC	254

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

TTCGATACAG GCAAACATGA ACTGCAGGAG GGTGGTGACG ATCATGATGT TGCGATGGT	60
CCGGATGGNC ACGAAGACGC ACTGGANCAC GTGCTTACGT CCTTTGCTC TGTTGATGGC	120
CCTGAGGGGA CGCAGGACCC TTATGACCCCT CAGAATCTTC ACAACGGGAG ATGGCACTGG	180
ATTGANTCCC ANTGACACCA GAGACACCCCA AACCACCAGN ATATCANTAT ATTGATGTAG	240
TTCCTGTAGA NGGCCCCCTT GTGGAGGAAA GCTCCATNAG TTGGTCATCT TCAACAGGAT	300
CTCAACAGTT TCCGATGGCT GTGATGGCA TAGTCATANT TAACCNTGTN TCGAA	355

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TAAGAGGGTA CCAGCAGAAA GGTTAGTATC ATCAGATAGC ATCTTATACG AGTAATATGC	60
CTGCTATTTG AAGTGTAAATT GAGAAGGAAA ATTTTAGCGT GCTCACTGAC CTGCCTGTAG	120
CCCCAGTGAC AGCTAGGATG TGCAATTCTCC AGCCATCAAG AGACTGAGTC AAGTTGTTCC	180
TTAAGTCAGA ACAGCAGACT CAGCTCTGAC ATTCTGATTC GAATGACACT GTTCAGGAAT	240
CGGAATCCTG TCGATTAGAC TGGACAGCTT GTGGCAAGTG AATTGCGCTG TAACAAGCCA	300
GATTTTTAA AATTATATATT GTAAATAATG TGTGTGTGTG TGTGTGTATA TATATATATA	360
TGTACAGTTA TCTAAGTTAA TTTAAAAGTT GTTTGGTACC CTCTTA	406

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TTTTTTTTTT TTTACTCGGC TCAGTCTAA CCTTTTGTA GTCACTCATA GGCCAGACTT	60
AGGGCTAGGA TGATGATTAA TAAGAGGGAT GACATAACTA TTAGTGGCAG GTTAGTTGTT	120

TGTAGGGCTC ATGGTAGGGG TAAAAGGAGG GCAATTCTA GATCAAATAA TAAGAAGGTA	180
ATAGCTACTA AGAAGAATT TATGGAGAAA GGGACGCGGG CGGGGGATAT AGGGTCAAG	240
CCGCACTCGT AAGGGGTGGA TTTTCTATG TAGCCGTTGA GTTGTGGTAG TCAAAATGTA	300
ATAATTATTA GTAGTAAGCC TAGGAGA	327

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TAGTCTATGC GGTTGATTG CCAATCCATT ATTTGCTGG A TTTGCTCATG TGTTTTGCCA	60
ATTGCATTCA TAATTTATTA TGCAATTATG CTTGTATCTC CTAAGTCATG GTATATAATC	120
CATGCTTTT ATGTTTGTC TGACATAAAC TCTTATCAGA GCCCTTGCA CACAGGGATT	180
CAATAAAAT TAACACAGTC TACATTATT TGGTGAATAT TGCAATCTG CTGTACTGAA	240
AGCACATTA GAAACAAAGG CAAGTGAGAA GAATGAAAAG CACTACTCAC AACAGTTATC	300
ATGATTGCGC ATAGACTA	318

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TCTTCAACCT CTACTCCCAC TAATAGCTTT TTGATGACTT CTAGCAAGCC TCGCTAACCT	60
CGCCTTACCC CCCACTATTAA ACCTACTGGG AGAACTCTCT GTGCTAGTAA CCACGTTCTC	120
CTGATCAAAT ATCACTCTCC TACTTACAGG ACTCAACATA CTAGTCACAG CCCTATACTC	180
CCTCTACATA TTTACCACAA CACAATGGGG CTCACTCACC CACCACATTA ACAACATAAA	240
ACCCTCATTC ACACGAGAAA ACACCCCTCAT GTTCATACAC CTATCCCCCA TTCTCCTCCT	300
ATCCCTAAC CCCGACATCA TTACCGGGTT TTCCTCTT	338

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

AGCCATTTAC CACCCATCCA CAAAAAAA AAAAAG AAAAATATCA AGGAATAAAA	60
ATAGACTTTG AACAAAAAGG AACATTGCT GGCCTGAGGA GGCATCACCC G	111

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TCGGGTGATG CCTCCTCAGG CCAAGAAGAT AAAGCTTCAG ACCCCTAACAA CATTTCAAA	60
AAGGAAGAAA GGAGAAAAAA GGGCATCATC CCCGTTCCGA AGGGTCAGGG AGGAGGAAAT	120
TGAGGTGGAT TCACGAGTTG CGGACAACTC CTTGATGCC AAGCGAGGTG CAGCCGGAGA	180
CTGGGGAGAG CGAGCCAATC AGGTTTGAA GTTCCTCTCA GTGC	224

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GCACTGAGAG GAACTTCGTT GGAAACGGGT TTTTTTCATG TAAGGCTAGA CAGAAGAATT	60
CTCAGTAAC T CTTGTGTT GTGTGTATT C AACTCACASA GTTGAACGAT CCTTTACACA	120
GAGCAGACTT G TAAACACTCT TWTGTGGAA TTTGCAAGTG GAGATTCAG SCGCTTGAA	180
GTSAAAGGTA GAAAAGGAAA TATCTTCCTA TAAAAACTAG ACAGAATGAT TCTCAGAAC	240
TCCTTGTGA TGTGTGCGTT CAACTCACAG AGTTAACCT TTCWTTTCAT AGAACAGTT	300
AGGAAACACT CTGTTGTAA AGTCTGCAAG TGGATAGAGA CCCTAACG	348

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GCACTGAGAG GAACTTCYTT GTGWTGKKG YATTCAACTC ACAGAGTTGA ASSWTSMTTT	60
ACABAGWKCA GGCTTKCAAA CACTTTTT GTMGAATYTG CAAGWGGAKA TTSRRCRC	120
TTTGWGGYCW WYSKTMGAAW MGGRWATATC TTCWYATMRA AMCTAGACAG AAKSATTCTC	180
AKAAWSTYYYY YTGTGAWGWS TGCRTTCAAC TCACAGAGKT KAACMWYCT KYTSATRGAG	240
CAGTTWKGAA ACTCTMTTTC TTTGGATTCT GCAAGTGGAT AGAGACCCTA ACG	293

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTCCTAGGCT

10

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AGTAGTTGCC

10

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TTCCGTTATG C

11

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TGGTAAAGGG

10

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCGGTCATAG

10

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TACAACGAGG

10

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TGGATTGGTC

10

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CTTTCTACCC

10

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TTTTGGCTCC

10

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GGAACCAATC

10

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCGATACAGG

10

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GGTACTAAGG

10

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

AGTCTATGCG

10

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CTATCCATGG

10

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCTGTCCACA

10

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

AAGAGGGTAC

10

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CTTCAACCTC

10

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

70

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GCTCCTCTTG CCTTACCAAC

20

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTAAGTCGAG CAGTGTGATG

20

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTAAGTCGAG CAGTCTGATG

20

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GACTTAGTGG AAAGAATGTA

20

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GTAATTCCGC CAACCGTAGT

20

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATGGTTGATC GATAGTGGAA

20

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

ACGGGGACCC CTGCATTGAG

20

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TATTCTAGAC CATTGCTAC

20

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

ACATAACCAC TTTAGCGTTC

20

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CGGGTGATGC CTCCTCAGGC

20

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

AGCATGTTGA GCCCAGACAC

20

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GACACCTTGT CCAGCATCTG

20

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

TACGCTGCAA CACTGTGGAG

20

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CGTTAGGGTC TCTATCCACT

20

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

AGACTGACTC ATGTCCCCTA

20

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TCATCGCTCG GTGACTCAAG

20

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

CAAGATTCCA TAGGCTGACC

20

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

ACGTACTGGT CTTGAAGGTC

20

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GACGCTTGGC CACTTGACAC

20

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GTATCGACGT AGTGGTCTCC

20

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

TAGTGACATT ACGACGCTGG

20

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CGGGTGATGC CTCCTCAGGC

20

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ATGGCTATTT TCGGGGGCTG ACA

23

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

CCGGTATCTC CTCGTGGGTA TT

22

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTGCCTGAGC CACAAATG

18

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

CCGGAGGAGG AAGCTAGAGG AATA

24

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TTTTTTTTTT TTAG

14

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Ser Ser Gly Gly Arg Thr Phe Asp Asp Phe His Arg Tyr Leu Leu Val
1 5 10 15
Gly Ile

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Gln Gly Ala Ala Gln Lys Pro Ile Asn Leu Ser Lys Xaa Ile Glu Val
1 5 10 15
Val Gln Gly His Asp Glu
20

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Ser Pro Gly Val Phe Leu Glu His Leu Gln Glu Ala Tyr Arg Ile Tyr
1 5 10 15
Thr Pro Phe Asp Leu Ser Ala
20

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Tyr Leu Leu Val Gly Ile Gln Gly Ala
1 5

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Gly Ala Ala Gln Lys Pro Ile Asn Leu
1 5

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Asn Leu Ser Lys Xaa Ile Glu Val Val
1 5

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Glu Val Val Gln Gly His Asp Glu Ser
1 5

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

His Leu Gln Glu Ala Tyr Arg Ile Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Asn Leu Ala Phe Val Ala Gln Ala Ala
1 5

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Phe Val Ala Gln Ala Ala Pro Asp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GCTCGCGGCC	GGCAGACTCAA	TTAACCCCTCA	CTAAAGGGAG	TCGACTCGAT	CAGACTGTTA	60
CTGTGTCTAT	GTAGAAAGAA	GTAGACATAA	GAGATTCCAT	TTTGTTCCTGT	ACTAAGAAAA	120
ATTCTTCTGC	CTTGAGATGC	TGTTAATCTG	TAACCCCTAGC	CCCAACCCCTG	TGCTCACAGA	180
GACATGTGCT	GTGTTGACTC	AAGGTTCAAT	GGATTAGGG	CTATGCTTTG	TTAAAAAAAGT	240
GCTTGAAGAT	AATATGCTTG	TTAAAAGTCA	TCACCATTCT	CTAATCTCAA	GTACCCAGGG	300
ACACAATACA	CTGCGGAAGG	CCGCAGGGAC	CTCTGTCTAG	GAAAGCCAGG	TATTGTCCAA	360
GATTCTCCC	CATGTGATAG	CCTGAGATAT	GGCCTCATGG	GAAGGGTAAG	ACCTGACTGT	420
CCCCCAGCCC	GACATCCCCC	AGCCCGACAT	CCCCCAGCCC	GACACCCGAA	AAGGGTCTGT	480
GCTGAGGAGG	ATTAGTAAAA	GAGGAAGGCC	TCTTTCAGT	TGAGGTAAGA	GGAAAGGCATC	540
TGTCTCTGC	TCGTCCTGG	GCAATAGAAT	GTCTTGGTGT	AAAACCCGAT	TGTATGTTCT	600
ACTTACTGAG	ATAGGAGAAA	ACATCCTAG	GGCTGGAGGT	GAGACACGCT	GGCGGCAATA	660
CTGCTCTTA	ATGCACCGAG	ATGTTGTAT	AAGTGCACAT	CAAGGCACAG	CACCTTCCT	720
TAAACTATT	TATGACACAG	AGACCTTTGT	TCACGTTTC	CTGCTGACCC	TCTCCCCACT	780
ATTACCTAT	TGGCCTGCCA	CATCCCCCTC	TCCGAGATGG	TAGAGATAAT	GATCAATAAA	840
TACTGAGGGA	ACTCAGAGAC	CAGTGTCCCT	GTAGGTCCCTC	CGTGTGCTGA	GCGCCGGTCC	900
CTTGGGCTCA	CTTTCTTTC	TCTATACCTT	GTCTCTGTGT	CTCTTTCTTT	TCTCAGTCTC	960
TCGTTCCACC	TGACGAGAAA	TACCCACAGG	TGTGGAGGGG	CAGGCCACCC	CTTCAATAAT	1020
TTACTAGCCT	GTTCGCTGAC	AACAAGACTG	GTGGTGCAGA	AGGTTGGTC	TTGGTGTTC	1080
CGGGGTGGCA	GGCATGGGCC	AGGTGGGAGG	GTCTCCAGCG	CCTGGTGCAA	ATCTCCAAGA	1140
AAGTGCAGGA	AACAGCACCA	AGGGTGATTG	AAATTGTTGA	TTTGGCGCGG	CAGGTAGCCA	1200
TTCCAGCGCA	AAAATGCGCA	GGAAAGCTTT	TGCTGTGCTT	GTAGGCAGGT	AGGCCCCAAG	1260
CACTTCTTAT	TGGCTAATGT	GGAGGGAACC	TGCACATCCA	TTGGCTGAAA	TCTCCGTCTA	1320
TTTGAGGCTG	ACTGAGCGCG	TTCCTTCTT	CTGTTGTTGCC	TGGAAACGGA	CTGTCGCT	1380
AGTAACATCT	GATCACGTTT	CCCATGGCC	GGCGTTCCG	GAAGCCCGCC	CTCCCATTT	1440
CGGAAGCTG	GGCAGAGTT	GGTCTGCAGG	TGGCCTCCAG	GTGCAAAGTG	GGAAAGTGTGA	1500
GTCCTCAGTC	TTGGGCTATT	CGGCCACGTG	CCTGCCGGAC	ATGGGACGCT	GGAGGGTCAG	1560
CAGCGTGGAG	TCCTGGCCTT	TTGCGTCCAC	GGGTGGGAAA	TTGGCCATTG	CCACGGCGGG	1620
AAACTGGGACT	CAGGCTGCC	CCCGGCCGTT	TCTCATCCGT	CCACCGGACT	CGTGGGCGCT	1680
CGCACTGGCG	CTGATGTAGT	TTCCTGACCT	CTGACCCGTA	TTGTCCTCAG	ATTAAGGTA	1740
AAAACGGGGC	TTTTTCAGCC	CACTCGGGTA	AAACGCCTT	TGATTCTAG	GCAGGTGTTT	1800
TGTTGCACGC	CTGGGAGGGA	GTGACCCGCA	GGTTGAGGT	TATTAATAA	CATTCCCTGGT	1860
TTATGTTATG	TTTATAATAA	AGCACCCCAA	CCTTACAAA	ATCTCACTTT	TTGCCAGTTG	1920
TATTATTTAG	TGGACTGTCT	CTGATAAGGA	CAGCCAGTTA	AAATGGAATT	TTGTTGTTGC	1980
TAATTAAACC	AATTTTAGT	TTTGGTGT	GTCCTAATAG	CAACAACCTC	TCAGGCTTTA	2040
TAAAACCATA	TTTCTGGGG	GAAATTCTG	TGTAAGGCAC	AGCGAGTTAG	TTTGAATTG	2100
TTTTAAAGGA	AGTAAGTCC	TGGTTTGAT	ATCTTAGTAG	TGTAATGCC	AACCTGGTTT	2160
TTACTAACCC	TGTTTTAGA	CTCTCCCTT	CCTTAAATCA	CCTAGCCTTG	TTTCCACCTG	2220
AATTGACTCT	CCCTTAGCTA	AGAGGCCAG	ATGGACTCCA	TCTTGGCTCT	TTCACTGGCA	2280
GCCCCCTCCT	CAAGGACTTA	ACTTGTGCAA	GCTGACTCCC	AGCACATCCA	AGAATGCAAT	2340
TAACTGTTAA	GATACTGTGG	CAAGCTATA	CCGCAGTCC	GAGGAATTCA	TCCGATTGAT	2400
TATGCCAAA	AGCCCCCGT	CTATCACCTT	GTAATAATCT	AAAGCCCT	GCACCTGGAA	2460
CTATTAACCTT	TCCGTAAAC	ATTATCCTT	TAACTTTT	TGCTTACTTT	ATTTCTGTAA	2520
AATTGTTTTA	ACTAGACCTC	CCCTCCCTT	TCTAAACCAA	AGTATAAAAG	AAGATCTAGC	2580
CCCTTCTTCA	GAGCGGAGAG	AATTTGAGC	ATTAGCCATC	TCTTGGCGGC	CAGCTAAATA	2640
AATGGACTTT	TAATTTGTC	CAAAGTGTGG	CGTTTCTCT	AACTCGCTCA	GGTACGACAT	2700

TTGGAGGCC	CAGCGAGAAA	CGTCACCGGG	AGAAACGTCA	CCGGCGAGA	GCCGGGCCG	2760
CTGTGTCTC	CCCCGGAAGG	ACAGCCAGCT	TGTAGGGGGG	AGTGCACCT	GAAAAAAA	2820
TTTCCAGGTC	CCCAAAGGGT	GACCCTTC	CGGAGGACAG	CGGATCGACT	ACCATGC3GG	2880
TGCCCACCAA	AATTCCACCT	CTGAGTCCTC	AACTGCTGAC	CCCCGGGTCA	GGTAGGTCAG	2940
ATTTGACTTT	GGTTCTGGCA	GAGGGAAGCG	ACCCCTGATGA	GGGTGTCCCT	CTTTTGACTC	3000
TGCCCATTT	TCTAGGATGC	TAGAGGGTAG	AGCCCTGGTT	TTCTGTTAGA	CGCCTCTGTG	3060
TCTCTGTCTG	GGAGGGAAGT	GGCCCTGACA	GGGGCCATCC	CTTGAGTCAG	TCCACATCCC	3120
AGGATGCTGG	GGGACTGAGT	CCTGGTTCT	GGCAGACTGG	TCTCTCTCTC	TCTCTTTTC	3180
TATCTCTAAT	CTTCCTTGT	TCAGGTTCT	TGGAGAATCT	CTGGGAAAGA	AAAAAGAAAA	3240
ACTGTTATAA	ACTCTGTGT	AATGGTGAAT	GAATGGGGGA	GGACAAGGGC	TTGCGCTTGT	3300
CCTCCAGTTT	GTAGCTCCAC	GGCGAAAGCT	ACGGAGTTCA	AGTGGGCCCT	CACCTGCGGT	3360
TCCGTGGCGA	CCTCATAAGG	CTTAAGGCAG	CATCCGGCAT	AGCTCGATCC	GAGCCGGGG	3420
TTTATACCGG	CCTGTCAATG	CTAAGAGGAG	CCCAAGTCCC	CTAAGGGGA	GCGGCCAGGC	3480
GGGCATCTGA	CTGATCCCCT	CACGGGACCC	CCTCCCCTTG	TTTGTCTAAA	AAAAAAA	3540
GAAGAAACTG	TCATAACTGT	TTACATGCCC	TAGGGTCAAC	TGTTGTTTT	ATGTTATTG	3600
TTCTGTTCGG	TGTCTATTGT	CTTGTAGT	GGTTGTCAAG	GTTTGATG	TCAGGACGTC	3660
GATATTGCC	AAGACGTCTG	GGTAAGAACT	TCTGCAAGGT	CCTTAGTGT	GATTTTTGT	3720
CACAGGAGGT	TAAATTCCTC	ATCAATCATT	TAGGCTGGCC	ACCACAGTCC	TGTCTTTCT	3780
GCCAGAAAGCA	AGTCAGGTGT	TGTTACGGGA	ATGAGTGTAA	AAAAACATTC	GCCTGATTGG	3840
GATTTCTGGC	ACCATGATGG	TTGTATTTAG	ATTGTCAAC	CCCACATCCA	GGTTGATTGG	3900
ACCTCCTCTA	AACTAAACTG	GTGGTGGGTT	AAAAACAGCC	ACCCCTGCAGA	TTTCCTTGCT	3960
CACCTCTTTG	GTCATTCTGT	AACTTTCTC	GTGCCCTTAA	ATAGCACACT	GTGTAGGGAA	4020
ACCTACCCCTC	GTACTGCTTT	ACTTCGTTA	GATTCTTACT	CTGTTCTCT	GTGGCTACTC	4080
TCCCACCTTA	AAAACGATCC	AAGTGGCTCT	TTTCCTCCTC	CCTGCCCCCT	ACCCCACACA	4140
TCTCGTTTTC	CAGTGCAGCA	GCAAGTTCA	CGTCTCCAGG	ACTTGGCTCT	GCTCTCACTC	4200
CTTGAACCC	AAAAAGAAAA	AGCTGGGTT	GAGCTATTG	CCTTGAGTC	ATGGAGACAC	4260
AAAAGGTATT	TAGGGTACAG	ATCTAGAAGA	AGAGAGAGAA	CACCTAGATC	CAACTGACCC	4320
AGGAGATCTC	GGGCTGGCCT	CTAGTCTCTC	TCCCTCAATC	TTAAAGCTAC	AGTGTAGTGG	4380
CAAGTGGTAT	TTAGCTGTT	TGGTTTTCT	GCTCTTC	GTCATGTTGA	TTCTGTTCTT	4440
TCGATACTCC	AGCCCCCCCAG	GGAGTGAGTT	TCTCTGTCTG	TGCTGGGTT	GATATCTATG	4500
TTCAAATCTT	ATTAAATTGC	CTTCAAAAAA	AAAAAAA	GGGAAACACT	TCCTCCCAGC	4560
CTTGTAAAGG	TTGGAGCCCT	CTCCAGTATA	TGCTGCAGAA	TTTTCTCTC	GGTTTCTCAG	4620
AGGATTATGG	AGTCCGCCTT	AAAAAAGGCA	AGCTCTGGAC	ACTCTGCAA	GTAGAATGGC	4680
CAAAGTTGG	AGTTGAGTGG	CCCCTTGAAG	GGTCACTGAA	CCTCACAATT	GTTCAAGCTG	4740
TGTGGCGGGT	TGTTACTGAA	ACTCCCCGCC	TCCCTGATCA	GTTTCCCTAC	ATTGATCAAT	4800
GGCTGAGTT	GGTCAGGAGC	ACCCCTTCCA	TGGCTCCACT	CATGCACCAT	TCATAATT	4860
ACCTCCAAGG	TCCTCCTGAG	CCAGACCGTG	TTTCGCCC	GACCCCTCAGC	CGGTTCACT	4920
CGCCCTGTAC	TGCCTCTCTC	TGAAGAAGAG	GAGAGTCTCC	CTCACCCAGT	CCCACCGCCT	4980
AAAAACCAGC	CTACTCCCTT	AGGGTCATCC	CATGTCTCT	CGGCTATGTC	CCCTGTAGGC	5040
TCATCACCCA	TTGCCTCTTG	GTTGCAACCG	GGTGGGAGG	AAAGTAGCCCC	TCTACTACCA	5100
CTGAGAGAGG	CACAAGTCCC	TCTGGGTGAT	GAGTGCTCCA	CCCCCTTCCT	GGTTTATGTC	5160
CCTTCTTCT	ACTTCTGACT	TGTATAATTG	AAAAACCCAT	AATCCTCCCT	TCTCTGAAAA	5220
GCCCCAGGCT	TTGACCTCAC	TGATGGAGTC	TGTACTCTGG	ACACATTGGC	CCACCTGGGA	5280
TGACTGTCAA	CAGCTCCTT	TGACCTTTT	CACCTCTGAA	GAGAGGGAAA	GTATCCAAAG	5340
AGAGGCCAAA	AACTACAACC	TCACATCAAC	CAATAGGCCG	GAGGAGGAAG	CTAGAGGAAT	5400
AGTGATTAGA	GACCCAATTG	GGACCTAATT	GGGACCCAAA	TTTCTCAAGT	GGAGGGAGAA	5460
CTTTTGACGA	TTTCCACCGG	TATCTCTCG	TGGGTATTCA	GGGAGCTGCT	CAGAACCTA	5520
TAAAATTGTC	TAAGGCGACT	GAAGTCGTCC	AGGGGCATGA	TGAGTCACCA	GGAGTGT	5580
TAGAGCACCT	CCAGGAGGCT	TATCGGATT	ACACCCCTT	TGACTGGCA	GCCCCCGAAA	5640
ATAGCCATGC	TCTTAATTG	GCATTGTTG	CTCAGGCAGC	CCCAGATAGT	AAAAGGAAAC	5700
TCCAAAAC	AGAGGGATT	TGCTGGAATG	AATACCA	AGCTTTAGA	GATAGCCTAA	5760
AAGGTTTTG	ACAGTCAGA	GGTTGAAAAA	CAAAACAAAG	CAGCTCAGGC	AGCTGAAAAA	5820
AGCCACTGAT	AAAGCATCCT	GGAGTATCAG	AGTTACTGT	TAGATCAGCC	TCATTTGACT	5880
TCCCCTCCCA	CATGGTGT	AAATCCAGCT	ACACTACTTC	CTGACTCAA	CTCCACTATT	5940
CCTGTTCATG	ACTGTCAGGA	ACTGTTGGAA	ACTACTGAAA	CTGGCCGACC	TGATCTCAA	6000

AATGTGCCCC	TAGGAAAGGT	GGATGCCACC	GTGTCACAG	ACAGTAGCAG	CTTCCTCGAG	6060
AAGGGACTAC	GAAAGGCCGG	TGCAGCTGTT	ACCATGGAGA	CAGATGTGTT	GTGGGCTCAG	6120
GCTTTACAG	CAAACACCTC	AGCACAAAG	GCTGAATTGA	TCGCCCTCAC	TCAGGCTCTC	6180
CGATGGGTA	AGGATATTAA	CGTTAACACT	GACAGCAGGT	ACGCCCTTGC	TACTGTGCAT	6240
GTACGTGGAG	CCATCTACCA	GGAGCGTGGG	CTACTCACCT	CAGCAGGTGG	CTGTAATCCA	6300
CTGTAAAGGA	CATCAAAAGG	AAAACACGGC	TGTTGCCCGT	GGTAACCAGA	AAGCTGATTC	6360
AGCAGCTCAA	GATGCAGTGT	GACTTCAGT	CACGCCTCTA	AACTTGCTGC	CCACAGTCTC	6420
CTTTCCACAG	CCAGATCTGC	CTGACAATCC	CGCATACTCA	ACAGAAGAAG	AAAAGTGGCC	6480
TCAGAACTCA	GAGCCAATAA	AAATCAGGAA	GGTTGGTGGA	TTCTTCCTGA	CTCTAGAAC	6540
TTCATACCCC	GAACTCTTGG	AAAAACTTTA	ATCAGTCACC	TACAGTCTAC	CACCCATTAA	6600
GGAGGAGCAA	AGCTACCTCA	GCTCCTCCGG	AGCCGTTTA	AGATCCCCCA	TCTTCAAAGC	6660
CTAACAGATC	AAGCAGCTCT	CCGGTGCACA	ACCTGCGCCC	AGGTAAATGC	CAAAAAAGGT	6720
CCTAAACCCA	GCCCAGGCCA	CCGTCTCCAA	AAAAACTCAC	CAGGAGAAAA	GTGGGAAATT	6780
GACTTTACAG	AACTAAAACC	ACACCGGGCT	GGGTACAAAT	ACCTTCTAGT	ACTGGTAGAC	6840
ACCTTCTCTG	GATGGACTGA	AGCATTGCT	ACCAAAACG	AAACTGTCAA	TATGGTAGTT	6900
AAGTTTTAC	TCAATGAAAT	CATCCCTCGA	CGTGGGCTGC	CTGTTGCCAT	AGGGTCTGAT	6960
AATGGACCGG	CCTTCGCCTT	GTCTATAGTT	TAGTCAGTCA	GTAAGGCGTT	AAACATTCAA	7020
TGGAAGCTCC	ATTGTGCCTA	TCGACCCCAG	AGCTCTGGGC	AAGTAGAACG	CATGAACCTGC	7080
ACCCCTAAAAA	ACACTCTTAC	AAAATTAAATC	TTAGAAACCG	GTGTAAATTG	TGTAAGTCTC	7140
CTTCCTTTAG	CCCTACTTAG	AGTAAGGTGC	ACCCCTTACT	GGGCTGGGTT	CTTACCTTT	7200
GAAATCATGT	ATGGGAGGGC	GCTGCCTATC	TTGCCTAACG	TAAGAGATGC	CCAATTGGCA	7260
AAAATATCAC	AAACTAATTAA	ATTACAGTAC	CTACAGTCTC	CCCAACAGGT	ACAAGATATC	7320
ATCCTGCCAC	TTGTTCGAGG	AACCCATCCC	AATCCAATT	CTGAACAGAC	AGGGCCCTGC	7380
CATTATTCC	CGCCAGGTGA	CCTGTGTTT	GTTAAAAGT	TCCAGAGAGA	AGGACTCCCT	7440
CCTGTTGGA	AGAGACCTCA	CACCGTCATC	ACGATGCCAA	CGGCTCTGAA	GGTGGATGGC	7500
ATTCTCGGT	GGATTCATCA	CTCCCCGCATC	AAAAAGGCCA	ACGGAGGCCA	ACTAGAAACA	7560
TGGGTCCCCA	GGGCTGGGTC	AGGCCCCTTA	AAACTGCACC	TAAGTTGGGT	GAAGCCATTA	7620
GATTAATTCT	TTTCTTAAT	TTTGTAAAAC	AATGCATAGC	TTCTGTCAAA	CTTATGTATC	7680
TTAAGACTCA	ATATAACCCC	CTTGTATATA	CTGAGGAATC	AATGATTG	TTCCCCAAAA	7740
ACACAAGTGG	GGAATGTAGT	GTCCAACCTG	GTCCCCACTA	ACCCGTGTTT	TAGACTCTCC	7800
CTTCCCTTTA	ATCACTCAGC	CTTGTTCCTA	CCTGAATTGA	CTCTCCCTTA	GCTAAGAGCG	7860
CCAGATGGAC	TCCATCTTGG	CTCTTCACT	GGCAGCCGCT	TCCTCAAGGA	CTTAACCTGT	7920
GCAAGCTGAC	TCCCAGCACA	TCCAAGAATG	CAATTAAC	ATAAGATACT	GTGGCAAGCT	7980
ATATCCGAG	TTCCCAGGAA	TTCGTCCAAT	TGATTACACC	AAAAAGCCCC	GCGTCTATCA	8040
CCTTGTAAATA	ATCTTAAAGC	CCCTGCACCT	GGAACATTAA	ACGTTCTGT	AACCATTAT	8100
CCTTTAACT	TTTTGCCTA	CTTTATTTCT	GTTAAATTGT	TTTAACTAGA	CCCCCCCTCT	8160
CCTTCTAAA	CCAAAGTATA	AAAGCAAATC	TAGCCCCCTC	TTCAGGCCGA	GAGAATTTCG	8220
AGCGTTAGCC	GTCTCTGGC	CACCAAGCTAA	ATAAACGGAT	TCTTCATGTG	TCTCAAAGTG	8280
TGGCGTTTTC	TCTAACTCGC	TCAGGTACGA	CCGTGGTAGT	ATTTTCCCCA	ACGTCTTATT	8340
TTTAGGGCAC	GTATGTAGAG	TAACCTTAT	AAAAGAAACC	AGTTAAGGAG	GTCCCCGGAT	8400
TTCCTTATC	AACTGTAATA	CTGGTTTGA	TTATTTATTT	ATTTATTTAT	TTTTTTTGAG	8460
AAGGAGTTTC	ACTCTGTTG	CCCAGGCTGG	AGTGAATGG	TGCGATCTTG	GCTCACTGCA	8520
ACTTCCGCCT	CCCAGGTTCA	AGCGATTCTC	CTGCCTCAGC	CTCGAGAGTA	GCTGGGATTA	8580
TAGGCATGCG	CCACCAACACC	CAGCTAATT	TGTATTTTA	GTAAAGATGG	GGTTTCTTCA	8640
TGTTGGTCAA	GCTGGTCTGG	AACTCCCCGC	CTCGGGTGAT	CTGCCCGCCT	CGGCCTCCGA	8700
AAGTGTGGG	ATTACAGGTG	TGATCCACCA	CACCCAGCCG	ATTTATATGT	ATATAAATCA	8760
CATTCCCTCA	ACAAAATGT	AGTGTTCCT	TCCATCTTGA	ATATAGGCTG	TAGACCCGT	8820
GGGTATGGGA	CATTGTTAAC	AGTGAGACCA	CAGCAGTTT	TATGTCATCT	GACAGCATCT	8880
CCAAATAGCC	TTCATGGTTG	TCACTGCTTC	CCAAGACAAT	TCCAAATAAC	ACTTCCCACT	8940
GATGACTTGC	TACTTGCTAT	TGTTACTAA	TGTGTTAAGG	TGGCTGTTAC	AGACACTATT	9000
AGTATGTCAG	GAATTACACC	AAAATTAGT	GGCTCAAACA	ATCATTTAT	TATGTATGTG	9060
GATTCTCATG	GTCAGGTCAG	GATTCAGAC	AGGGCACAAAG	GGTAGCCAC	TTGTCTCTGT	9120
CTATGATGTC	TGGCCTCAGC	ACAGGAGACT	CAACAGCTGG	GGTCTGGGAC	CATTTGGAGG	9180
CTTGTCCCT	CACATCTGAT	ACCTGGCTTG	GGATGTTGGA	AGAGGGGGTG	AGCTGAGACT	9240
GAGTGCCAT	ATGTAGTGT	TCCATATGGC	CTTGACTTCC	TTACAGCCTG	GCAGCCTCAG	9300

GGTAGTCAGA ATTCTTAGGA GGCACAGGGC TCCAGGGCAG ATGCTGAGGG GTCTTTATG	9360
AGGTAGCACA GCAAATCCAC CCAGGATC	9388

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 419 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TGTAAGTCGA GCAGTGTGAT GGAAGGAATG GTCTTGAG AGAGCATATC CATCTCCTCC	60
TCACTGCCTC CTAATGTCAT GAGGTACACT GAGCAGAATT AAACAGGGTA GTCTTAACCA	120
CACTATTTT AGCTACCTTG TCAAGCTAAT GGTAAAGAA CACTTTGGT TTACACTTGT	180
TGGGTCTAG AAGTTGCTTT CCGCCATCAC GCAATAAGTT TGTGTGTAAT CAGAAGGAGT	240
TACCTTATGG TTTCAGTGTGTC ATTCTTAGT TAACTTGGGA GCTGTGTAAT TTAGGCTTG	300
CGTATTATTT CACTCTGTG CTCCACTTAT GAAGTGATTG TGTGTTCGCG TGTGTGTGCG	360
TGCGCATGTG CTTCCGGCAG TTAACATAAG CAAATACCCA ACATCACACT GCTCGACTT	419

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TGTAAGTCGA GCAGTGTGAT GTCCACTGCA GTGTGTTGCT GGGAACAGTT AATGAGCAAA	60
TTGTATACAA TGGCTAGTAC ATTGACCGGG ATTGTTGAA GCTGGTGAGT GTTATGACTT	120
AGCCTGTTAG ACTAGTCTAT GCACATGGCT CTGGTCAACT ACCGCTCTCT CATTCTCCA	180
GATAAAATCCC CCATGCTTTA TATTCTCTTC CAAACATACT ATCCTCATCA CCACATAGTT	240
CCTTTGTTAA TGCTTTGTT TAGACTTTCC CTTTCTGTT TTCTTATTCA AACCTATATC	300
TCTTTGCATA GATTGTAAT TCAAATGCC TCAGGGTGCA GGCAGTTCAT GTAAGGGAGG	360
GAGGCTAGCC AGTGAGATCT GCATCACACT GCTCGACTTA CA	402

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TCGGGTGATG CCTCCTCAGG CCAAGAAGAT AAAGCTTCAG ACCCCTAACCA CATTTCAAA	60
AAGGAAGAAA GGAGAAAAAA GGGCATCATC CCCGTTCCGA AGGGTCAGGG AGGAGGAAAT	120
TGAGGTGGAT TCACGAGTTG CGGACAACTC CTTTGATGCC AAGCGAGGTG CAGCCGGAGA	180

CTGGGGAGAG CGAGCCAATC AGGTTTGAA GTTCCTCTCA GTGC

224

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

AGCCATTAC CACCCATCCA CAAAAAAAAG AAAAAAAG AAAAATATCA AGGAATAAAA	60
ATAGACTTG AACAAAAAGG AACATTTGCT GGCCTGAGGA GGCATCACCC G	111

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

TAGCATGTTG AGCCCAGACA CTTGTAGAGA GAGGAGGACA GTTAGAAGAA GAAGAAAAGT	60
TTTAAATGC TGAAAGTTAC TATAAGAAAG CTTGGCTTT GGATGAGACT TTTAAAGATG	120
CAGAGGATGC TTTGCAGAAA CTTCATAAAAT ATATGCAGGT GATTCTTAT TTCTCTCTAG	180
AAATTTAGTG ATATTTGAAA TAATGCCAA ACTTAATTCTT CTCCTGAGGA AAACATATTCT	240
ACATTACTTA AGTAAGGCAT TATGAAAAGT TTCTTTTAG GTATAGTTT TCCTAATTGG	300
GTTTGACATT GCTTCATAGT GCCTCTGTTT TTGTCCATAA TCGAAAGTAA AGATAGCTGT	360
GAGAAAACCA TTACCTAAAT TTGGTATGTT GTTTTGAGAA ATGTCCTTAT AGGGAGCTCA	420
CCTGGTGGTT TTTAAATTAT TGTTGCTACT ATAATTGAGC TAATTATAAA AACCTTTTG	480
AGACATATTG TAAATTGCT TTTCTGTAA TACTGATGAT GATTTTCT CATGCATTTT	540
CTTCTGAATT GGGACCATTG CTGCTGTGTC TGGGCTCACCA TGCTA	585

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TAGCATGTTG AGCCCAGACA CTGGGCAGCG GGGGTGGCCA CGGCAGCTCC TGCCGAGCCC	60
AAGCGTGTGTT GTCTGTGAAG GACCCTGACG TCACCTGCCA GGCTAGGGAG GGGTCAATGT	120
GGAGTGAATG TTCAACCGACT TTGCGCAGGAG TGTGCAGAAAG CCAGGTGCAA CTTGGTTG	180
TTGTGTTCAT CACCCCTCAA GATATGCACA CTGCTTTCCA AATAAAGCAT CAACTGTCAT	240
CTCCAGATGG GGAAGACTTT TTCTCCAACC AGCAGGCAGG TCCCCATCCA CTCAGACACC	300
AGCACGTCCA CCTTCTCGGG CAGCACCACG TCCTCCACCT TCTGCTGGTA CACGGTGATG	360

ATGTCAGCAA AGCCGTTCTG CANGACCAGC TGCCCCGTGT GCTGTGCCAT CTCACTGGCC	420
TCCACCGCGT ACACCGCTCT AGGCCGCGCA TANTGTGCAC AGAANAAATG ATGATCCAGT	480
CCCACAGCCC ACGTCCAAGA NGACTTTATC CGTCAGGGAT TCTTTATTCT GCAGGGATGAC	540
CTGTGGTATT AATTGTTCGT GTCTGGGCTC AACATGCTA	579

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TGACACCTTG TCCAGCATCT GCAAGCCAGG AAGAGAGTCC TCACCAAGAT CCCCACCCCG	60
TTGGCACCAAG GATCTTGGAC TTCCAATCTC CAGAACTGTG AGAAATAAGT ATTTGTCGCT	120
AAATAAATCT TTGTGGTTTC AGATATTTAG CTATAGCAGA TCAGGCTGAC TAAGAGAAAC	180
CCCATAAGAG TTACATACTC ATTAATCTCC GTCTCTATCC CCAGGTCTCA GATGCTGGAC	240
AAGGTGTCA	249

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TGACACCTTG TCCAGCATCT GCTATTTGT GACTTTTAA TAATAGCCAT TCTGACTGGT	60
GTGAGATGGT AACTCATTGT GGGTTGGTC TGCATTTCTC TAATGATCAG TGATATTAAG	120
CTTTTTTAA ATATGCTTGT TGACCACATG TATATCATCT TTTGAGAAGT GTCTGTTCAT	180
ATCCTTGCC CACTTTTAA TTTTTTATC TTGTAAATTG GTTTAATTTC CTTACAGATG	240
CTGGACAAGG TGTCA	255

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

TTACGCTGCA ACACTGTGGA GGCCAAGCTG GGATCACTTC TTCATTCTAA CTGGAGAGGA	60
GGGAAGTTCA AGTCCAGCAG AGGGTGGGTG GGTAGACAGT GGCACTCAGA AATGTCAGCT	120
GGACCCCTGT CCCCGCATAG GCAGGACAGC AAGGCTGTGG CTCTCCAGGG CCAGCTGAAG	180
AACAGGACAC TGTCTCCGCT GCCACAAAGC GTCAGAGACT CCCATCTTG AAGCACGGCC	240
TTCTTGGTCT TCCTGCACTT CCCTGTTCTG TTAGAGACCT GGTTATAGAC AAGGCTTCTC	300

CACAGTGTG CAGCGTAA

318

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

TNACGCNGCN ACNNTGTAGA GANGGNAAGG CNTTCCCCAC ATTNCCCCTT CATNANAGAA	60
TTATTTCNACC AAGNNTGACC NATGCCNTT ATGACTTACA TGCNNACTNC NTAATCTGTN	120
TCNNNGCCTTA AAAGCENNNTC CACTACATGC NTCANCACTG TNTGTGTNAC NTCATNAACT	180
GTCNGNAATA GGGGNCNATA ACTACAGAAA TGCANTTCAT ACTGCTTCCA NTGCCATCNG	240
CGTGTGGCCT TNCCTACTCT TCTTNTTATTC CAAGTAGCAT CTCTGGANTG CTTCCCCACT	300
CTCCACATTG TTGCAGCNAT AAT	323

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

TCAAGATTCC ATAGGCTGAC CAGTCCAAGG AGAGTTGAAA TCATGAAGGA GAGTCTATCT	60
GGAGAGAGCT GTAGTTTGA GGGTTGCAAA GACTTAGGAT GGAGTTGGTG GGTGTGGTTA	120
GTCTCTAAAGG TTGATTTGT TCATAAATTT CATGCCCTGA ATGCCTTGCT TGCCTCACCC	180
TGGTCCAAGC CTTAGTGAAC ACCTAAAAGT CTCTGTCTTC TTGCTCTCCA AACTTCTCCT	240
GAGGATTTC CTCAGATTGTC TACATTCAAGA TCGAAGCCAG TTGGCAAACA AGATGCAGTC	300
CAGAGGGTCA G	311

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CAAGATTCCA TAGGCTGACC AGGAGGCTAT TCAAGATCTC TGGCAGTTGA GGAAGTCTCT	60
TTAAGAAAAT AGTTTAAACA ATTTGTTAAA ATTTTTCTGT CTTACTTCAT TTCTGTAGCA	120
GTTGATATCT GGCTGTCTT TTTATAATGC AGAGTGGGAA CTTTCCCTAC CATGTTGAT	180
AAATGTTGTC CAGGCTCCAT TGCCAATAAT GTGTTGTCCA AAATGCCTGT TTAGTTTTA	240
AAGACGGAAC TCCACCCCTT GCTTGGTCTT AAGTATGTAT GGAATGTTAT GATAGGACAT	300
AGTAGTAGCG GTGGTCAGCC TATGGAATCT TG	332

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TCAAGATTCC ATAGGCTGAC	CTGGACAGAG ATCTCCTGGG	TCTGGCCCAG GACAGCAGGC	60
TCAAGCTCAG TGGAGAAGGT	TTCCATGACC CTCAGATTCC	CCCAAACCTT GGATTGGGTG	120
ACATTGCATC TCCTCAGAGA	GGGAGGAGAT GTANGTCTGG	GCTTCACAG GGACCTGGTA	180
TTTTAGGATC AGGGTACCGC	TGGCCTGAGG CTTGGATCAT	TCAAGCCTG GGGGTGGAAT	240
GGCTGGCAGC CTGTGGCCCC	ATTGAAATAG GCTCTGGGGC	ACTCCCTCTG TTCCTANTTG	300
AACTTGGGTA AGGAACAGGA	ATGTGGTCAN CCTATGGAAT	CTTGA	345

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GACGCTTGGC CACTTGACAC	ATTAAACAGT TTTGCATAAT	CACTANCATG TATTCTAGT	60
TTGCTGCTG CTGTGATGCC	CTGCCCTGAT TCTCTGGCGT	TAATGATGGC AAGCATAATC	120
AAACGCTGTT CTGTTAAC	CAAGTTATAA CTGGCATTGA	TTAAAGCATT ATCTTCACA	180
ACTAAACTGT TCTTCATANA	ACAGCCCCATA TTATTATCAA	ATTAAGAGAC AATGTATTCC	240
AATATCCTT ANGGCCAATA	TATTTNATGT CCCTTAATTA	AGAGCTACTG TCCGT	295

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GACGCTTGGC CACTTGACAC	TGCAGTGGGA AAACCAGCAT	GAGCCGCTGC CCCCAAGGAA	60
CCTCGAAGCC CAGGCAGAGG	ACCAGCCATC CCAGCCTGCA	GGTAAAGTGT GTCACCTGTC	120
AGGTGGGCTT GGGGTGAGTG	GGTGGGGAA GTGTGTGTG	AAAGGGGGTG TNAATGTNTA	180
TGCGTGTGAG CATGAGTGAT	GGCTAGTGTG ACTGCATGTC	AGGGAGTGTG AACAAAGCGTG	240
CGGGGGTGTG TGTCAAGTG	CGTATGCATA TGAGAATATG	TGTCTGTGGA TGAGTGCATT	300
TGAAAGTCTG TGTGTGTGCG	TGTGGTCATG ANGGTAANTT	ANTGACTGCG CAGGATGTGT	360
GAGTGTGCAT GGAACACTCA	NTGTGTGTGT CAAGTGGCCN	ANCAGTC	406

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

TGACGCTTGG CCACTTGACA CACTAAAGGG TGTTACTCAT CACTTTCTTC TCTCCTCGGT	60
GGCATGTGAG TGCATCTATT CACTTGGCAC TCATTTGTTT GGCAGTGACT GTAANCCANA	120
TCTGATGCAT ACACCAAGCTT GTAAATTGAA TAAATGTCTC TAATACTATG TGCTCACAAT	180
ANGGTANGGG TGAGGAGAAG GGGAGAGA	208

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CTTCAACCTC CTTCAACCTC CTTCAACCTC CTGGATTCAA ACAATCATCC CACCTCAGAC	60
TCCTTAGTAG CTGAGACTAC AGACTCACGC CACTACATCT GGCTAAATT TTGTAGAGAT	120
AGGGTTTCAT CATGTTGCC TGGCTGGTCT CAAACTCCTG ACCTCAAGCA ATGTGCCAC	180
CTCAGCCTCC CAAAGTGTG GGATTACAGG CATAAGCCAC CATGCCAGT CCATNTTTAA	240
TCTTCCCTAC CACATTCTTA CCACACTTTC TTTTATGTTT AGATACATAA ATGCTTACCA	300
TTATGATACA ATTGCCACA GTATTAAGAC AGTAACATGC TGACACAGGT TGTCAGCTAG	360
GAACAGTAGG CAATACCACA TAGCTTAGGT GTGTGGTAGA CTATACCATC TAGGTTTGTG	420
TAAGTTACAC TTTATGCTGT TTACACAATG ACAAAACCAC CTAATGATGC ATTTCTCAGA	480
ATGTATCCTT GTCAAGTAAGC TATGATGTAC AGGGAACACT GCCCAAGGAC ACAGATATTG	540
TACCTGT	547

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GCTCCTCTTG CCTTACCAAC TCACCCAGTA TGTCAGCAAT TTTATCRGCT TTACCTACGA	60
AACAGCCTGT ATCCAAACAC TTAACACACT CACCTGAAAA GTTCAGGCAA CAATCGCCTT	120
CTCATGGGTC TCTCTGCTCC AGTTCTGAAC CTTTCTCTTT TCCTAGAACAA TGCATTARG	180
TCGATAGAACAG TTCCCTCTCAG TGC	203

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

TGTAAGTCGA	GCAGTGTGAT	GGGTGGAACA	GGGTTGTAAG	CAGTAATTGC	AAACTGTATT	60
TAAACAAATAA	TAATAATATT	TAGCATTAT	AGAGCACTTT	ATATCTCAA	AGTACTTGCA	120
AACATTAYCT	AATTAATAC	CCTCTCTGAT	TATAATCTGG	ATACAAATGC	ACTTAAACTC	180
AGGACAGGGT	CATGAGARAA	GTATGCATT	GAAAGTTGGT	GCTAGCTATG	CTTTAAAAAC	240
CTATACAATG	ATGGGRAAGT	TAGAGTTCA	ATTCTGTTGG	ACTGTTTTG	TGCATTCAG	300
TTCAGCCTGA	TGGCAGAATT	AGATCATATC	TGCACTCGAT	GACTYTGCTT	GATAACTTAT	360
CACTGAAATC	TGAGTGTGA	TCATCACACT	GCTCGACTTA	CA		402

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

AGCATGTTGA	GCCAGACAC	TGACCAGGAG	AAAAACCAAC	CAATAGAAAC	ACGCCAGAC	60
ACTGACCAGG	AGAAAAACCA	ACCAATAAAA	ACAGGCCGG	ACATAAGACA	AATAATAAAA	120
TTAGCGGACA	AGGACATGAA	AACAGCTATT	GTAAGAGCGG	ATATAAGTGGT	GTGTGTCTGG	180
GCTCAACATG	CTA					193

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

TGTTGAGCCC	AGACACTGAC	CAGGAGAAAA	ACCAACCAAT	AAAAACAGGC	CCGGACATAA	60
GACAAATAAT	AAAATTAGCG	GACAAGGACA	TGAAAACAGC	TATTGTAAGA	GCGGATATAG	120
TGGTGTGTGT	CTGGGCTCAA	CATGCTA				147

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

TAGCATGTTG AGCCCAGACA CAAATCTTC CTTAAGCAAT AAATCATTTC TGCATATGTT	60
TTTAAAACCA CAGCTAAGCC ATGATTATTC AAAAGGACTA TTGTATTGGG TATTTGATT	120
TGGGTTCTTA TCTCCCTCAC ATTATCTTCA TTTCTATCAT TGACCTCTTA TCCCAGAGAC	180
TCTCAAACCTT TTATGTTATA CAAATCACAT TCTGTCTCAA AAAATATCTC ACCCACTTCT	240
CTTCTGTTTC TGCGTGTGTA TGTGTGTG TGCTAACAT GCTA	294

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CGGGATTGGC TTTGAGCTGC AGATGCTGCC TGTGACCGCA CCCGGCGTGG AACAGAAAGC	60
CACCTGGCTG CAAGTGCGCC AGAGCCGCC TGACTACGTG CTGCTGTGGG GCTGGGGCGT	120
GATGAACTCC ACCGCCCTGA AGGAAGCCCA GGCCACCGGA TACCCCCGCG ACAAGATGTA	180
CGGCGTGTGG TGGGCCGGTG CGGAGCCCGA TGTGCGTGAC GTGGGCGAAG GCGCCAAGGG	240
CTACAAACGCG CTGGCTCTGA ACGGCTACGG CACGCAGTC AAGGTGATCC ANGACATCCT	300
GAAACACGTG CACGACAAGG GCCAGGGCAC GGGGCCAAA GACGAAGTGG GCTCGGTGCT	360
GTACACCCGC GGCGTGATCA TCCAGATGCT GGACAAGGTG TCAATCACTA AT	412

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

TTGACACCTT GTCCAGCCTC TGCATCTGAT GAGAGCCTCA GATGGCTACC ACTAATGGCA	60
GAAGGCAAAG GAGAACAGGC ATTGTATGGC AAGAAAGGAA GAAAGAGAGA GGGGAGAAAG	120
GTGCTAGGTT CTTTCAACA ACCAGTTCTT GATGGAAC TG AGAGTAAGAG CTCAAGGCCA	180
GGTGTGGTGA CTCCAACCAG TAATCCCAAC ATTTTAGGAG GCTGAGGCAG GCAGATGTC	240
TGACCCCATG AGTTGTGAC CAGCCTGAAC AACATCATGA GACTCCATCT CTACAATAAT	300
TACAAAAATT AATCAGGCAT TGTGGTATGC CCTGTAGTC CAGATGCTGG ACAAGGTGTC	360
A	361

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

TWGACTGACT	CATGTCCTT	ACACCCAACT	ATCTTCTCCA	GGTGGCCAGG	CATGATAGAA	60
TCTGATCTG	ACTTAGGGGA	ATATTTCTT	TTTACTTCCC	ATCTTGATTC	CCTGCCGGTG	120
AGTTTCCTGG	TTCAGGGTAA	GAAAGGAGCT	CAGGCCAAAG	TAATGAACAA	ATCCATCCTC	180
ACAGACGTAC	AGAATAAGAG	AACWTGGACW	TAGCCAGCAG	AACMCAAKTG	AAAMCAGAAC	240
MCTTAMCTAG	GATRACAAMC	MCRRARATAR	KGCYCMCMC	WTATAATAGA	AACCAAACCTT	300
GTATCTAATT	AAATATTTAT	CCACYGTCAG	GGCATTAGTG	GTGGTATGAA	ATACGCTTTG	360
GCTAGGATTC	CTGAGGTTAG	AATGGAARAA	CAATTGCAMC	GAGGGTAGGG	GACATGAGTC	420
AKTCTAA						427

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

AACGTCGCAT	GCTCCGGCC	GCCATGGCG	CGGGATAGAC	TGACTCATGT	CCCCTAAGAT	60
AGAGGAGACA	CCTGCTAGGT	GTAAGGAGAA	GATGGTTAGG	TCTACGGAGG	CTCCAGGGTG	120
GGAGTAGTTC	CCTGCTAAGG	GAGGGTAGAC	TGTTCAACCT	GTTCCCTGCTC	CGGCCTCCAC	180
TATAGCAGAT	GCGAGCAGGA	GTAGGAGAGA	GGGAGGTAAG	AGTCAGAACG	TTATGTTGTT	240
TATGCGGGGA	AACGCCRTAT	CGGGGGCAGC	CRAGTTATTA	GGGGACANTR	TAGWYARTCW	300
AGNTAGCATC	CAAAGCGNGG	GAGTTNTCCC	ATATGGTTGG	ACCTGCAGGC	GGCCGCATTA	360
GTGATTAGCA	TGTGAGCCCC	AGACACGCAT	AGCAACAAGG	ACCTAAACTC	AGATCCTGTG	420
CTGATTACTT	AACATGAATT	ATTGTATTTA	TTTAACAAC	TTGAGTTATG	AGGCATATTA	480
TTAGGTCCAT	ATTACCTGGA					500

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

TTCATCGCTC	GGTGACTCAA	GCCTGTAATC	CCAGAACTTT	GGGAGGCCGA	GGGGAGCAGA	60
TCACCTGAGG	TTGGGAGTTT	GAGACCAGCC	TGCCAACAT	GGTGACAAACC	CGTCTCTGCT	120
AAAAATACAA	AAATTAGCCA	AGCATGGTGG	CATGCACTTG	TAATCCCAGC	TACTCGGGAG	180
GCTGAGGCAG	GAGAATCACT	TGAGGCCAGG	AGGCAGAGGT	TGCAGTGAGG	CAGAGGTTGA	240
GATCATGCCA	CTGCACTCCA	GCCTGGCAA	CAGAGTAAGA	CTCCATCTCA	AAAAAAA	300
AAAAAAAGAA	TGATCAGAGC	CACAAATACA	GAAAACCTTG	AGTCACCGAG	CGATGAAA	358

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

TTCTGTCCAC	ACCAATCTTA	GAGCTCTGAA	AGAATTGTC	TTTAAATATC	TTTTAATAGT	60
AACATGTATT	TTATGGACCA	AATTGACATT	TTCGACTATT	TTTTCCCAA	AAAAGTCAGG	120
TGAATTCAG	CACACTGAGT	TGGGAATTTC	TTATCCCAGA	AGWCGGCACG	AGCAATTCA	180
TATTTATTAA	AGATTGATTC	CATACTCCGT	TTTCAAGGAG	AATCCCTGCA	GTCTCCTTAA	240
AGGTAGAACCA	AATACTTTCT	ATTTTTTTT	CACCATTGTG	GGATTGGACT	TTAAGAGGTG	300
ACTCTAAAAA	AACAGAGAAC	AAATATGTCT	CAGTTGTATT	AAGCACGGAC	CCATATTATC	360
ATATTCACTT	AAAAAAATGA	TTTCCTGTGC	ACCTTTGGC	AACTTCTCTT	TCATGTAG	420
GGAAAAACTT	AGTCACCCCTG	AAAACCACA	AAATAAAATAA	AACTTGTAGA	TGTGGCAGA	480
ARGTTGGGG	GTGGACATTG	TATGTGTTA	AATTAAACCC	TGTATCACTG	AGAAGCTGTT	540
GTATGGGTCA	GAGAAAATGA	ATGCTTAGAA	CCTGTTACCA	TCTTCAAGAG	CAGAAGCAAA	600
CCACATGTCT	CAGCTATATT	ATTATTATT	TTTTATGCAT	AAAGTGAATC	ATTTCTCTG	660
TATTAATTTC	CAAAGGGTTT	TACCCCTCTAT	TTAAATGCTT	TGAAAAACAG	TGCATTGACA	720
ATGGGTTGAT	ATTTTTCTTT	AAAAGAAAAA	TATAATTATG	AAAGCCAAGA	TAATCTGAAG	780
CCTGTTTAT	TTTAAAACCTT	TTTATGTTCT	GTGGTTGATG	TTGTTTGT	GTGTTTCT	840
ATTTTGTGG	TTTTTACTT	TGTTTTTGT	TTTGTGTTG	TTTGGTTDG	CATACTACAT	900
GCAGTTCTT	TAACCAATGT	CTGTTGGCT	AATGTAATTA	AAAGTGTAA	TTTATATGAG	960
TGCATTTCAA	CTATGTCAAT	GGTTCTTAA	TATTTATTGT	GTAGAAGTAC	TGGTAATTT	1020
TTTATTTACA	ATATGTTAA	AGAGATAACA	GTGTTGATATG	TTTCATGTG	TTTATAGCAG	1080
AAGTTATTTA	TTCTCTATGGC	ATTCCAGCGG	ATATTTGGT	GTGCGAGG	CATGCAGTCA	1140
ATATTTGTA	CAGTTAGTGG	ACAGTATTCA	GCAACGCCTG	ATAGCTTCTT	TGGCCTTATG	1200
TTAAATAAAA	AGACCTGTTT	GGGATGTAAA	AAAAAAA	AAAAAAA	AAAAAAA	1260
AAAAAA						1265

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

TGTAAGTCGA	GCAGTGTGAT	GACGATATT	TTCTTATTAA	TGTGGTAATT	GAACAAATGA	60
TCTGTGATAC	TGATCCTGAG	CTAGGAGGCG	CTGTTCAAGTT	AATGGGACTT	CTTCGTACTC	120
TAATTGATCC	AGAGAACATG	CTGGCTACAA	CTAATAAAAC	CGAAAAAAAGT	GAATTTCCTAA	180
ATTTTTCTA	CAACCATTGT	ATGCATGTC	TCACAGCACC	ACTTTGACC	AATACTTCAG	240
AAGACAAATG	TGAAAAGGAT	AATATAGTTG	GATCAAACAA	AAACAAACACA	ATTGTCCCG	300
ATAATTATCA	AACAGCACAG	CTACTTGCT	TAATTTAGA	GTTACTCACA	TTTTGTGTGG	360
AACATCACAC	TGCTCGACTT	ACA				383

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

TGGGCACCTT	CAATATCGCA	AGTTAAAAAT	AATGTTGAGT	TTATTATACT	TTTGACCTGT	60
TTAGCTAAC	AGGGTGAAGG	CATGTAAGA	ATGTGGACTT	CTGAGGAATT	TTCTTTTAAA	120
AAGAACATAA	TGAAGTAACA	TTTAATTAC	TCAAGGACTA	CTTTGGTTG	AAGTTTATAA	180
TCTAGATACC	TCTACTTTT	GTFFFFGCTG	TTCGACAGTT	CACAAAGACC	TTCAGCAATT	240
TACAGGGTAA	AATCGTTGAA	GTAGTGGAGG	TGAAACTGAA	ATTTAAAATT	ATTCTGTAAA	300
TACTATAGGG	AAAGAGGCTG	AGCTTAGAAT	CTTTGGTTG	TTCATGTGTT	CTGTGCTCTT	360
ATCATCACAC	TGCTCGACTT	ACA				383

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

TCGGGTGATG	CCTCCTCAGG	CTTGTGTTA	GTGTACACAG	AGCTGCTCAT	GAAGCGACAG	60
CGGCTGCC	TGGCACTTCA	GAACCTCTTC	CTCTACACTT	TTGGTGCCT	TCTGAATCTA	120
GGTCTGCATG	CTGGCGGCCG	CTCTGGCCCA	GGCCTCCTGG	AAAGTTCTC	AGGATGGGCA	180
GCACACTCGTGG	TGCTGAGCCA	GGCACTAAAT	GGACTGCTCA	TGTCTGCTGT	CATGGAGCAT	240
GGCAGCAGCA	TCACACGCC	CTTTGTGGTG	TCCTGCTCGC	TGGTGGTCAA	CGCCGTGCTC	300
TCAGCAGTCC	TGCTACGGCT	GCAGCTCACA	GCCGCCTTCT	TCCTGGCCAC	ATTGCTCATT	360
GGCCTGGCCA	TGCGCCTGTA	CTATGGCAGC	CGCTAGTCCC	TGACAACCTC	CACCCCTGATT	420
CCGGACCCG	TAGATTGGGC	GCCACCA	GATCCCCCTC	CCAGGCCCTTC	CTCCCCCTCTCC	480
CATCAGCGGC	CCTGTAACAA	GTGCCTTGTG	AGAAAAGCTG	GAGAAGTGAG	GGCAGCCAGG	540
TTATTCTCTG	GAGGGTGGTG	GATGAAGGGG	TACCCCTAGG	AGATGTGAAG	TGTGGGTTG	600
GTAAAGGAAA	TGCTTACCAT	CCCCCACCCC	CAACCAAGTT	NTTCCAGACT	AAAGAATTAA	660
GGTAACATCA	ATACCTAGGC	CTGAGGAGGC	ATCACCCGA			699

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

TCGGGTGATG	CCTCCTCAGG	CCAGATCAA	CTTGGGGTTG	AAAAGTGTG	AAAGAAATCA	60
ATGTCGGAGA	AAGAATTTC	CAAAAGAAAA	ATGCCTAATC	AGTACTAATT	TAATAGGTCA	120

CATTAGCAGT	GGAAGAAGAA	ATGTTGATAT	TTTATGTCAG	CTATTGATA	ATCACCAGAG	180
TGCTTAGCTT	CATGTAAGCC	ATCTCGTATT	CATTAGAAAT	AAGAACAAATT	TTATTCGTCG	240
GAAAGAACCTT	TTCAATTAT	AGCATCTAA	TTGCTCAGGA	TTTAAATTT	TGATAAAGAA	300
AGCTCCACTT	TTGGCAGGAG	TAGGGGCAG	GGAGAGAGGA	GGCTCCATCC	ACAAGGACAG	360
AGACACCAGG	GCCAGTAGGG	TAGCTGGTGG	CTGGATCAGT	CACAACGGAC	TGACTTATGC	420
CATGAGAAGA	AACAACCTCC	AAATCTCAGT	TGCTTAATAC	AACACAAGCT	CATTTCTTGC	480
TCACGTTACA	TGTCCTATGT	AGATCAACAG	CAGGTGACTC	AGGGACCCAG	GCTCCATCTC	540
CATATGAGCT	TCCATAGTCA	CCAGGACACG	GGCTCTGAAA	GTGTCTCCA	TGCAGGGACA	600
CATGCCTCTT	CCTTCATTG	GGCAGAGCAA	GTCACTTATG	GCCAGAAGTC	ACACTGCAGG	660
GCAGTGCCAT	CCTGCTGTAT	GCCTGAGGAG	GCATCACCCCG	A		701

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 700 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

TCGGGTGATG	CCTCCTCANG	CCCCTAAATC	AGAGTCCAGG	GTCAGAGCCA	CAGGAGACAG	60
GGAAAGACAT	AGATTTAAC	CGGCCCCCTT	CAGGAGATTC	TGAGGCTCAG	TTCACTTTGT	120
TGCAGTTTGA	ACAGAGGCAG	CAAGGCTAGT	GGTTAGGGGC	ACGGTCTCTA	AAGCTGCAC	180
GCCTGGATCT	GCCTCCCAGC	TCTGCCAGGA	ACCAAGCTGCC	TGGCCTTGAG	CTGCTGACAC	240
GCAGAAAGCC	CCCTGTGGAC	CCAGTCCTCCT	CGTCTGTAAG	ATGAGGACAG	GACTCTAGGA	300
ACCCCTTCCC	TTGGTTTGGC	CTCACTTTCA	CAGGCTCCCA	TCTTGAACTC	TATCTACTCT	360
TTTCCTGAAA	CCTTGTAAAA	AAAAAAAGTG	CTAGCCTGGG	CAACATGGCA	AAACCTGTC	420
TCTACAAAAA	ATACAAAAAT	TAGTTGGGTG	TGGTGGCATG	TGCCTGTAGT	CCCAGCCACT	480
TGGGAGGTGC	TGAGGTGGGA	GGATCACTTG	AGCCCGGGAG	GTGGAGGTTG	CAGTGAGCCA	540
AGATCATGCC	ACTGCACCTCC	AGCCTGAGTA	ATAGAGTAAG	ACTCTGTCTC	AAAAACAACA	600
ACAACAACAG	TGAGTGTGCC	TCTGTTCCG	GGTTGGATGG	GGCACACAT	TTATGCATCT	660
CTCAGATTG	GACGCTGCAG	CCTGAGGAGG	CATCACCCGA			700

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

TATAGGGCGA	ATTGGGCCCG	AGTTGCATGN	TCCCGGCCGC	CATGGCCGCG	GGATTCGGGT	60
GATGCCTCCT	CAGGCTTGTC	TGCCACAAGC	TACTTCTCTG	AGCTCAGAAA	GTGCCCTCTG	120
ATGAGGGAAA	ATGTCCTACT	GCACTGCGAA	TTTCTCAGTT	CCATTGTTACC	TCCCAGTCCT	180
CCTTCTAAC	CAGTTAATAA	ATTCATCCA	CAAGTATTAA	CTGATTACCT	GCTTGTGCCA	240
GGGACTATTC	TCAGGCTGAA	GAAGGTGGGA	GGGGAGGGCG	GAACCTGAGG	AGCCACCTGA	300
GCCAGCTTTA	TATTTCACC	ATGGCTGGCC	CATCTGAGAG	CATCTCCCCA	CTCTCGCCAA	360
CCTATCGGGG	CATAGCCCCAG	GGATGCCCCC	AGGCAGGCCCA	GGTTAGATGC	GTCCCTTTGG	420
CTTGTCACTG	ATGACATACA	CCTTAGCTGC	TTAGCTGGTG	CTGGCCTGAG	GAGGCATCAC	480
CCGA						484

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

TCGGGTGATG CCTCCTCAGG GCTCAAGGGA TGAGAAGTGA CTTCTTCTG GAGGGACCGT	60
TCATGCCACC CAGGATGAAA ATGGATAGGG ACCCACTTGG AGGACTTGCT GATATGTTG	120
GACAAATGCC AGGTAGCGGA ATTGGTACTG GTCCAGGAGT TATCCAGGAT AGATTTCAC	180
CCACCATGGG ACGTCATCGT TCAAATCAAC TCTTCAATGG CCATGGGGGA CACATCATGC	240
CTCCCACACA ATCGCAGTTT GGAGAGATGG GAGGCAAGTT TATGAAAAGC CAGGGGCTAA	300
GCCAGCTCTA CCATAACCAG AGTCAGGGAC TCTTATCCCA GCTGCAAGGA CAGTCGAAGG	360
ATATGCCACC TCGGTTTCT AAGAAAGGAC AGCTTAATGC AGATGAGATT AGCCTGAGGA	420
GGCATCACCC GA	432

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

TAGCATGTTG AGCCCAGACA CAGTAGCATT TGTGCCAATT TCTGGTTGGA ATGGTGACAA	60
CATGCTGGAG CCAAGTGCTA ACATGCCATTG GTTCAAGGGA TGGAAAGTCA CCCGTAAGGA	120
TGGCAATGCC AGTGGAACCA CGCTGCTTGA GGCTCTGGAC TGCATCCTAC CACCAACTCG	180
CCCAACTGAC AAGCCCTTGC GCCTGCCTCT CCAGGATGTC TACAAAATTG GTGGTATTGG	240
TACTGTTCTT GTTGGCCGAG TGGAGACTGG TGGTCTCAAA CCCGGTATGG TGGTCACCTT	300
TGCTCCAGTC AACGTTACAA CGGAAGTAAA ATCTGTCGAA ATGCACCATG AAGCTTGAG	360
TGAAGCTCTT CCTGGGGACA ATGTGGGCTT CAATGTCAAG AATGTGTCTG TCAAGGATGT	420
TCGTCGTGGC AACGTTGCTG GTGACAGCAA AAATGACCCA CCAATGGAAG CAGCTGGCTT	480
CACTGCTCAG GTGATTATCC TGAACCATCC AGGCCAAATA AGTGGCGCT ATGCCCTGT	540
ATTGGATTGC CACACGGCTC ACATTGCTATG CAAGTTGCT GAGCTGAAGG AAAAGATTGA	600
TCGCCGTCTT GGTAAGGAGTGG CCCTAAATTG TTGAAGTCTG GTGATGCTGC	660
CATTGTTGAT ATGGTTCTG GCAAGCCCAT GTGTGTTGAG AGCTTCTCAG ACTATCCACC	720
TTTGGGTCGC TTTGCTGTTG GTGATATGAG ACAGACAGTT GCGGTGGGTG TCTGGGCTCA	780
ACATGCTA	788

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

TAGCATGTTG	AGCCCAGACA	CCTGTGTTTC	TGGGAGCTCT	GGCAGTGGCG	GATTCA TAGG	60
CACTTGGGCT	GCACCTTGAA	TGACACACTT	GGCTTTATTA	GATTCACTAG	TTTTTAAAAA	120
ATTGTTGTTG	CTTTCTTTTC	ATTAAAGGTT	TAATCAGACA	GATCAGACAG	CATAATTTG	180
TATTTAATGA	CAGAAACGTT	GGTACATTTG	TTCATGAATG	AGCTTGCATT	CTGAAGCAAG	240
AGCCTACAAA	AGGCACTTGT	TATAAATGAA	AGTTCTGGCT	CTAGAGGCCA	GTACTCTGGA	300
GTTTCAGAGC	AGCCAGTGT	TGTTCCAGTC	AGTGATGCCT	AGTTATATAG	AGGAGGAGTA	360
CACTGTGCAC	TCTTCTAGGT	GTAAGGGTAT	GCAACTTTGG	ATCTTAAAAT	TCTGTACACA	420
TACACACTTT	ATATATATGT	ATGTATGTAT	GAAAACATGA	AATTAGTTTG	TCAAATATGT	480
GTGTGTTAG	TATTTTAGCT	TAGTGCAACT	ATTCCACAT	TATTTATTAA	ATTGATCTAA	540
GACACTTCT	TGTTGACACC	TTGAATATTA	ATGTTCAAGG	GTGCAATGTG	TATTCCCTTA	600
GATTGTTAAA	GCTTAATTAC	TATGATTTGT	AGTAAATTAA	CTTTTAAAAT	GTATTTGAGC	660
CCITTCTGTAG	TGTCGTAGGG	CTCTTACAGG	GTGGGAAAGA	TTTTAATTTT	CCAGTTGCTA	720
ATTGAACAGT	ATGGCCTCAT	TATATATTTC	GATTTATAGG	AGTTTGTGTC	TGGGCTCAAC	780
					ATGCTA	786

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

TAGCATGTTG	AGCCCAGACA	CTGGTTACAA	GACCAGACCT	GCTTCCTCCA	TATGTAACAA	60
GCTTTAAAAA	AGCCAGTGA	CCTTTTAAT	ACTTTGGCAA	CCTTCTTCA	CAGGCAAAGA	120
ACACCCCCAT	CCGCCCCTTG	TTGGAGTGC	AGAGTTGGC	TTGGTTCTT	TGCCTTGCC	180
GGAGTATACT	TCTAATTCT	GTTGCTCTGC	ACAAGCTGAA	TACCGAGCTA	CCCACCGCCA	240
CCCAGGCCAG	GTTCACACTC	ATTTATTACT	TTATGTTCT	GTTCCATTGC	TGGTCCACAG	300
AAATAAGTTT	TCCTTGGAG	GAATGTGATT	ATACCCCTTT	AATTCCCTCC	TTTGCTTTT	360
TTTTAATATC	ATTGGTATGT	GTGGGCCA	GAGGAAACTG	AAATTCAACCA	TCATCTTGAC	420
TGGCAATCCC	ATTACCATGC	TTTTTTAAA	AAACGTAATT	TTTCTGCT	TACATTGGCA	480
GAGTAGCCCT	TCCTGGCTAC	TGGCTTAATG	TAGTCACTCA	GTGGCTAGGT	GGCATTAGGC	540
ATGAGACCTG	AAGCACAGAC	TGTCTTACCA	CAAAGGTGA	CAAGATCTCA	AACCTTAGCC	600
AAAGGGCTAT	GTCAGGTTTC	AATGCTATCT	GCTTCTGTT	CTGCTCACTG	TTCTGGATT	660
TGTCTCTT	CATCCCTAGC	ACCAGAATT	CCCAGTCTCC	CTCCCTACCT	TCCCTGTT	720
TAATTCTAAT	CTATCAGCAA	AATAACTTT	CAAATGTTT	AACCGGTATC	TCCATGTGTC	780
					TGGGCTCAAC	796

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GGATGTGCTG CAAGGCAGATT AAGTTGGGTA ACGCCAGGGT TTTCCCAGTC ACGACGTTGT	60
AAAACGACGG CCAGTGAATT GTAATACGAC TCACTATAGG GCGAATTGGG CCCGACGTCG	120
CATGCTCCCG GCCCCATGG CGCGGGATA GCATGTTGAG CCCAGACACC TGCAGGTCA	180
TTGGAGAGAT TTTTCACGTT ACCAGCTTGA TGGTCTTTT CAGGAGGAGA GACACTGAGC	240
ACTCCCAAGG TGAGGTTGAA GATTTCTCT AGATAGCCGG ATAAGAAGAC TAGGAGGGAT	300
GCCTAGAAAA TGATTAGCAT GCAAATTCT ACCTGCCATT TCAGAACTGT GTGTCAGCCC	360
ACATTCAAGCT GCTTCTTGTG AACTGAAAAG AGAGAGGTAT TGAGACTTTT CTGATGGCCG	420
CTCTAACATT GTAACACAGT AATCTGTGTG TGTGTGGGTG TGTGTGTGTG TCTGGGCTCA	480
ACATGCTA	488

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TAGCATGTTG AGCCCAGACA CGGCGACGGT ACCTGATGAG TGGGGTGATG GCACCTGTGA	60
AAAGGAGGAA CGTCATCCCC CATGATATTG GGGACCCAGA TGATGAACCA TGGCTCCGCG	120
TCAATGCATA TTTAATCCAT GATACTGCTG ATTGGAAGGA CCTGAACCTG AAGTTTGTGC	180
TGCAGGTTTA CGGGACTAT TACCTCACGG GTGATCAAAA CTTCCTGAAG GACATGTGGC	240
CTGTGTGTCT AGTAAGGGAT GCACATGCAG TGGCCAGTGT GCCAGGGTA TGGTTGGTGT	300
CTGGGCTCAA CATGCTA	317

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TAGCATGTTG AGCCCAGACA CTGGCTGTTA GCCAAATCCT CTCTCAGCTG CTCCCTGTGG	60
TTTGGTGACT CAGGATTACA GAGGCATCCT GTTTCAGGGA ACAAAAAGAT TTTAGCTGCC	120
AGCAGAGAGC ACCACATACA TTAGAATGGT AAGGACTGCC ACCTCCTTCA AGAACAGGAG	180
TGAGGGTGGT GGTGAATGGG AATGGAAGCC TGCATTCCCT GATGCATTTG TGCTCTCTCA	240
AATCCTGTCT TAGTCTTAGG AAAGGAAGTA AAGTTTCAAG GACGGTTCCG AACTGCTTT	300
TGTGTCTGGG CTCAACATGC TATCCCGCGG CCATGGCGGC CGGGAGCATG CGACGTCGGG	360
CCCAATTTCGC CCTATAGTGA GTCGTATTAC AATTCACTGG CCGTCGTTTT ACAACGTCGT	420
GACTGGAAA ACCCTGGCGT TACCCAACCTT AATCGCCTTG CAGCACATCC CCCTTTCCCA	480
GCTGGCGTAA TANCGAAAAG GCGCGCA	507

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GATTTACGCT GCAACACTGT GGAGGTAGCC CTGGAGCAAG GCAGGCATGG ATGCTTCTGC	60
AATCCCCAAA TGGAGCCTGG TATTCAGCC AGGAATCTGA GCAGAGCCCC CTCTAATTGT	120
AGCAATGATA AGTTATTCTC TTTGTTCTTC AACCTTCAA TAGCCTTGAG CTTCCAGGGG	180
AGTGTCTTA ATCATTACAG CCTGGTCTCC ACAGTGTGAG CGCGTAA	227

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

TTACGCTGCA ACAGTGTGGA GCAGATTAAC ATCAGACTTT TCTATCAACA TGACTGGGGT	60
TACTAAAAAG ACAACAAATC AATGGCTTCA AAAGTCTAAG GAATAATTTC GATACTTCAA	120
CTTTATAAAA CCTGACAAAA CTATCAATCA AGCATAAAGA CAGATGAAGA ACATTTCCAG	180
ATTTTGGCCA ATCAGATATT TTACCTCCAC AGTGTGAG CGTAA	225

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GGCCCGACGT CGCATGCTCC CGGCCGCCAT GGCGCGGGG TTCGTTAGGG TCTCTATCCA	60
CTGGGACCCA TAGGCTAGTC AGAGTATTG GAGTTGAGTT CCTTCTGCT TCCCAGAATT	120
TGAAAGAAAA GGAGTGTGGT GATAGAGCTG AGAGATCAGA TTTGCCTCTG AAGCCTGTC	180
AAGATGTATG TGCTCAGACC CCACCACTGG GGCGCTGTGGG TGAGGTCCTG GGCATCTATT	240
TGAATGAATT GCTGAAGGGG AGCACTATGC CAAGGAAGGG GAACCCATCC TGGCACTGGC	300
ACAGGGGTCA CCTTATCCAG TGCTCAGTGC TTCTTTGCTG CTACCTGGTT TTCTCTCATA	360
TGTGAGGGGC AGGTAAAGAAG AAGTGCCRG TGGTGTGCGA GTTTAGAAC ATCTACCAAGT	420
AAGTGGGAA GTTCACAAA GCAGCAGCTT TGTGAGGAGT ATTTTCACCT TCAGTTAGAA	480
GAGGAAGGCT GTGAGATGAA TGTTAGTTGA GTGGAAAAGA CGGGTAAGCT TAGTGGATAG	540
AGACCTAAC GAATCACTAG TGCAGCGGCC TTGCAGGTGCG ACCATATGGG AGAGCTC	597

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GGCCCAGGT TGCATGTTCC CGGCCGCAT GGCCGCGGGA TTCGTTAGGG TCTCTATCCA	60
CTACCTAAAA AATCCCAAAC ATATAACTGA ACTCCTCACCA CCCAATTGGA CCAATCCATC	120
ACCCCAGAGG CCTACAGATC CTCCCTTGAT ACATAAGAAA ATTTCCCAA ACTACCTAAC	180
TATATCATT TGCAAGATTT GTTTTACCAA ATTTTGATGG CCTTTCTGAG CTTGTCAGTG	240
TGAACCACTA TTACGAACGA TCGGATATTA ACTGCCCCTC ACCGTCCAGG TGTAGCTGGC	300
AACATCAAGT GCAGTAAATA TTCATTAAGT TTTCACCTAC TAAGGTGCTT AAACACCCCTA	360
GGGTGCCATG TCGGTAGCAG ATCTTTGAT TTGTTTTAT TTCCCATAAAG GGTCTGTTC	420
AAGGTCAATC ATACATGTAG TGTGAGCAGC TAGTCACTAT CGCATGACTT GGAGGGGTGAT	480
AATAGAGGCC TCCTTTGCTG TTAAAGAACT CTTGTCCCAG CCTGTCAAAG TGGATAGAGA	540
CCCTAACGAA TCACTAGTGC GGCGCCTGC AGGTCGACCA TATGGGAGAG CTCCCAA	597

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

TCGTTAGGGT CTCTATCCAC TTGCAGGTAA AATCCAATCC TGTGTATATC TTATAGTCTT	60
CCATATGTAG TGGTCAAGA GACTGCAGTT CCAGAAAGAC TAGCCGAGCC CATCCATGTC	120
TTCCACTTAA CCCTGCTTTG GGTTACACAT CTAACTTTT CTGTTCAAGT TTCTCTGTGT	180
AGTTTATAGC ATGAGTATTG GGAWAATGCC CTGAAACCTG ACATGAGATC TGGGAAACAC	240
AAACTTACTC AATAAGAATT TCTCCCATAT TTTTATGATG GAAAAATTTC ACATGCACAG	300
AGGAGTGGAT AGAGACCTA ACGA	324

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GCGCGGGGAT TCGGGGTGAT ACCTCCTCAT GCCAAAATAC AACGTNTAAT TTCACAACCTT	60
GCCTTCCAAT TTACGCATTT TCAATTGCT CTCCCCATTT GTTGAGTCAC AACAAACACC	120
ATTGCCAGA AACATGTATT ACCTAACATG CACATACTCT TAAAACTACT CATCCCTT	178

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TGACACCTTG TCCAGCATCT GACACAGTCT TGGCTCTTGG AAAATATTGG ATAAATGAAA	60
ATGAATTTCT TTAGCAAGTG GTATAAGCTG AGAATATAACG TATCACATAT CCTCATTCTA	120
AGACACATTC AGTGTCCCTG AAATTAGAAT AGGACTTACA ATAAGTGTGT TCACCTTCCTC	180
AATAGCTGTT ATTCAATTGA TGGTAGGCCT TAAAAGTCAA AGAAATGAGA GGGCATGTGA	240
AAAAAAAGCTC AACATCACTG ATCATTAGAA AACTTCCATT CAAACCCCCA ATGAGATACC	300
ATCTCATACC AGTCAGAATG GCTATTATTA AAAAGTCAAA AAATAACAGA TGCTGGACAA	360
GGTGTCA	367

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GACACCTTGT CCAGCATCTG ACAACGCTAA CAGCCTGAGG AGATCTTTAT TTATTTATTT	60
AGTTTTTACT CTGGCTAGGC AGATGGTGGC TAAAACATTC ATTTACCCAT TTATTCACTT	120
AATTGTTCTC GCAAGGCCTA TGGATAGAGT ATTGTCCAGC ACTGCTCTGG AAGCTAGGAG	180
CATGGGGATG AACAAAGATAG GCTACATCCT GTTCCCACAG AACTTCCACT TTAGTCTGGG	240
AAACAGATGA TATATAACAAA TATATAAATG AATTCAAGGTA GTTTTAAGTA CGAAAAGAAT	300
AAGAAAGCAG AGTCATGATT TANAATGCTG GAAACAGGGG CTATTGCTTG AGATATTGAA	360
GGTGCCCCAA	369

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

TGACACCTTG TCCAGCATCT GCACAGGGAA AAGAAACTAT TATCAGAGTG AACAGGCAAC	60
CTACAGAATG GGAGAAAATT TTTGCAATCT ATCCATCTGA CAAAGGGCTA ATATCCAGAA	120
TCTACAAAGA ACTTATACAA ATTTACAAGA AACAAACAAA CAAACAACTC CTCAAAAAGT	180
GGGTGAAGGA TGTGAACAGA CACTTCTCAA AAGAAGACAT TTATGGGCC AACAAACATA	240
TGAAAAAAAG CTCATCATCA CTGGTCACTA GATAAAATGCA AATCAAAACC ACAATGAGAT	300
ACCATCTCAT TCCAGTTAGA ATGGCAATCA TTAAAAAGTC AGGAAACAAAC AGATGCTGGA	360
CAAGGTGTC	369

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 449 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

TGACGCTTGG CCACATTGACA CTTCATCTT GCACAGAAAA ACTTCTTAC AGATTTAATT	60
CAAGACTGGT CTAGTGACAG TCCTCCAGAC ATTTTTCAT TTGTTCCATA TACGTGGAAT	120
TTTAAAATCA TGTTTCATCA GTTTGAAATG ATTTGGGCTG CTAATCAACA CAATTGGATC	180
GACTGTTCTA CTAACACAACA GGAAAATGTG TATCTGGCAG CCTGTGGAGA AACACTAAAC	240
ATTGATTTT CTTGCCCTT TACGGACTTT GTTCCAGCTA CATGTAATAC CAAGTTCTCT	300
TTAAGAGGAG AAGATGTTGA TCTTCATTTG TTTCTACCAAG ACTGCCACCC TAGTAAATAT	360
TCTTATTAA TGCTGGTAAA AAATTGCCAT CCAAATAAGA TGATTCATGA TACTGGTATT	420
CCTGCTGAGT GTCAAGTGGC CAAGCGTCA	449

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

TGACGCTTGG CCACATTGACA CCAGGGATGT AKCAGTTGAA TATAATCCTG CAATTGTACA	60
TATTGGCAAT TTCCCATCAA ACATTCTAGA AAGAGACAAAC CAGGATTGCT AGGCCATAAA	120
AGCTGCAATA AATAACTGGT AATTGAGTA ATCATTTCAG GCCAATTCAA TCCAGTTGG	180
CTCAGAGGTG CCTTGGCTG AGAGAAGAGG TGAGATATAA TGTGTTTCT TGCAACTTCT	240
TGGAAGAATA ACTCCACAAT AGTCTGAGGA CTAGATACAA ACCTATTGTC CATTAAAGCA	300
CCAGAGTCTG TTAATTCCAG TACTGATAAG TGTTGGAGAT TAGACTCCAG TGTGTCAAGT	360
GGCCAAGCGT CA	372

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

TGACGCTTGG CCACATTGACA CTTATGTAGA ATCCATCGTG GGCTGATGCA AGCCCTTAT	60
TTAGGCTTAG TGTTGGGGC ACCTTCATAA TCACACTAGA GACAAACGCC ACAAGATCTG	120
CAGAAACATT CAGTTCTGAN CACTCGAATG GCAGGATAAC TTTTGTGTT GTAATCCTTC	180
ACATATACAA AAACAAACTC TGCANTCTCA CGTTACAAA AAACGTACTG CTGTAAAATA	240
TTAAGAAGGG GTAAAGGATA CCATCTATAA CAAAGTAAC TACAACTAGT GTCAAGTGGC	300
CAAGCGTCA	309

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

TGACGCTTGG CCAC TTGACA CCCA ATCTCG CACTTCATCC TCCCAGCACC TGATGAAGTA	60
GGACTGCAAC TATCCCCACT TCCCAGATGA GGGGACCAAN GTACACATTA GGACCCGGAT	120
GGGAGCACAG ATTTGTCCGA TCCCAGACTC CAAGCACTCA GCGTCACTCC AGGACAGCGG	180
CTTTCAGATA AGGTACACAAA CATGAATGGC TCCGACAAACC GGAGTCAGTC CGTGCTGAGT	240
TAAGGCAATG GTGACACCGA TGCACGTGTN ACCTGTAATG GTTCATCGTA AGTGTCAAGT	300
GGCCAAGCGT CA	312

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

TGTATCGACG TAGTGGTCTC CTCAGCCATG CAGAACTGTG ACTCAATTAA ACCTCTTCC	60
TTTATGAATT ACCCAATCTC GGGTAGTGTCT TTTATAGTAG TGTGAGAATG GACTAATACA	120
AGTACATTTT ACTTAGTAAT AATAATAAAC AAATATATTA CATTGGTGTG TATTTACTAC	180
ACCATATTTT TTATTGTTAT TGTAGTGTAC ACCTTCTACT TATTAAGA AATAGGCCCG	240
AGGCAGGGCAG ATCACGAGGT CAGGAGATGG AGACCCTAC GTCGATAC	288

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTGGGCACCT TCAATATCAT GACAGGTGAT GTGATAACCA AGAAGGCTAC TAAGTGATTA	60
ATGGGTGGGT AATGTATACA GAGTAGGTAC ACTGGACAGA GGGGTAATTC ATAGCCAAGG	120
CAGGAGAACG AGAATGGCAA AACATTTCAT CACACTACTC AGGATAGCAT GCAGTTAAA	180
ACCTATAAGT AGTTTATTTT TGGAAATTTC CACTTAATAT TTTCAGACTG CAGGTAACTA	240
AACTGTGGAA CACAAGAACAA TAGATAAGGG GAGACCACTA CGTCGATAC	289

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GTATCGACGT AGTGGTCTCC CAAGCAGTGG GAAGAAAACG TGAACCAATT AAAATGTATC	60
AGATACCCCA AAGAAAGGCG CTTGAGTAAA GATTCCAAGT GGGTCACAAT CTCAGATCTT	120
AAAATTCAGG CTGTCAAAGA GATTTGCTAT GAGGTTGCTC TCAATGACTT CAGGCACAGT	180
CGGCAGGAGA TTGAAGCCCT GGCCATTGTC AAGATGAAGG AGCTTTGTGC CATGTATGGC	240
AAGAAAGACC CCAATGAGCG GGACTCCTGG AGACCACTAC GTCGATAC	288

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GCTTTTGGG AAAAACNCAA NTGGGGAAA GGGGGNTNN TNGCAAGGGG ATAAAGGGG	60
AANCCCAGGG TTTCCCCATT CAGGGAGGTG TAAAAAGNCG GCCAGGGGAT TGTAANAGGA	120
TTCAATAATA GGGGAATGG GCCCNGAAGT TGCAAGGTT CNGCCCGCCA TGNCCGCGGG	180
ATTTAGTGAC ATTACGACGS TGGTAATAAA GTGGGSCCAA WAAATATTG TGATGTGATT	240
TTTSGACCAAG TGAAACCCATT GWACAGGACC TCATTTCTY TGAGATGRTA GCCATAATCA	300
GATAAAAGRT TAGAAGTYTT TCTGCACGTT AACAGCATCA TTAAATGGAG TGGCATCACC	360
AATTCACCC TTTGTTAGCC GATACCTTCC CCTTGAAGGC ATTCAATTAA GTGACCAATC	420
GTCATACGAG AGGGGATGGC ATGGGGATTG ATGATGATAT CAGGGGTGAT ACCTTCACAG	480
GTGAAAGGCA TATCCTCTTG TCTATACTGA ATACCACAAG TACCCCTTTG ACCATGTCGA	540
CTAGCAAATT TGTCTCCAAT CTGTGTWATC CCTAACAGAG CGTACCCCTTA TTTTACAAAA	600
TTTATATCCT TCCTGATTGA GAGTTACCAT AACCTGATCC ACAATGCCCG TCTCGCTWGT	660
TCTGAGAAAA GTGCTACAGT CTCTCTGGT ATAGCGTCTA TTGGTGCTCT CCAATTCACTC	720
TTCATTTTC AGGCAAGGTG AACTGTTTG CCTATAATAA CMTCATCTCC TGATACMCGA	780
AACCCCKGGA RCTATCAAAC CATCATCATC CAGCGTTCKT WATGTYMCTA AATCCCTATT	840
GCGGCCGCT GCAGGTCAAC ATATNGAAA ACCCCCCACC CCTTNGGAGC NTACCTGAA	900
TTTTCCATAT GTCCCNTAAA TTANCTNGNC TTANCCTGGC CNTAACCTNT TCCGGTTAA	960
ATTGTTCCG CCCCCNTTCC CCNCCTNNNA ACCGGAAACC TTAATTTNA ACCNGGGTT	1020
CCTATCC	1027

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

AGTGACATTA CGACGCTGGC CATCTTGAAT CCTAGGGCAT GAAGTTGCC CAAAGTTCA	60
CACTTGGTTA AGCCTGATCC CTCTGGTTA TCACAAAGAA TAGGATGGGA TAAAGAAAGT	120
GGACACTTAA ATAAGCTATA AATTATATGG TCCTTGTCTA GCAGGAGACA ACTGCACAGG	180

TATACTACCA GCGTCGTAAT GTCACTA

207

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TGGGCACCTT CAATATCTAT TAAAAGCACA AATACTGAAG AACACACCAA GACTATCAAT	60
GAGGTTACAT CTGGAGTCCT CGATATATCA GGAAAAAATG AAGTGAACAT TCACAGAGTT	120
TTACTTCTTT GGGAACTCAA ATGCTAGAAA AGAAAAGGGT GCCCTCTTTC TCTGGCTTCC	180
TGGTCCTATC CAGCGTCGTA ATGTCACTA	209

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

NTACGCTGCA ACACTGTGGA GCCACTGGTT TTTATTCCCG GCAGGTTATC CAGCAAACAG	60
TCACTGAACA CACCGAAGAC CGTGGTATGG TAACC GTTCA CAGTAATCGT TCCAGTCGTC	120
TGCAGGGACCC CGACGAGCGT CACTGGGTAC AGACCAGATT CAGCCGGAAG AGAAAGCGCC	180
GCAGGGAGAG ACTCGAACTC CACTCCGCTG GTGAGCAGCC CCATGTTTTC AACTCGAAGT	240
TCAAACGGCA TTGGGTTATA TACCATCAGC TGAACATTCAC ACACATCTCC TTGAACCCAC	300
TGGAAATCTA TTTCTTGTT CCGCTCTTCT CCACAGTGTT GCAGCGTAA	349

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TGCTCCTCTT GCCTTACCAA CCCAAAGCCC ACTGTGAAAT ATGAAGTGAA TGACAAAATT	60
CAGTTTCAA CGCAAATATAG TATAGTTAT CTGATTCTTT TGATCTCCAG GACACTTTAA	120
ACAACTGCTA CCACCAACCAC CAACCTAGGG ATTTAGGATT CTCCACAGAC CAGAAATTAT	180
TTCTCCTTGT AGTTTCAGGC TCCTCTGGGA CTCCTGTTCA TCAATGGGTG GTAAATGGCT	240
A	241

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TAGCCATTAA CCACCCATCT GCAAACCSWG ACMWWCARGR CYWGWACKYA GGCGATTG	60
AGTACTGGTA ATGCTCTGAT CATGTTAGTT ACATAAGTGT GGTCAAGTTA CAAAAATTCA	120
CAGAACTAAA TACTCAATGC TATGTGTTCA TGTCTGTGTT TATGTGTGTT TAATGTTCA	180
ATTAAGTTTT TTAAAGGGAGG AGAGATGATT TCCAAATAAG AAAGCCGTGT TGGTAAGGCA	240
AGAGGAGC	248

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TACGCTGCAA CACTGTGGAG CCATTCTACAG AGGTCCCTAA TTAAGGAACA AGTGATTATG	60
CTACCTTGC ACGGTTAGGG TACCGCGGCC GTTAAACATG TGTCACTGGG CAGGCGGTGC	120
CTCTAATACT GGTGATGCTA GAGGTGATGT TTTTGGTAAA CAGGGGGGGT AAGATTGCC	180
GAGTCCCTT TACCTTTTT AACCTTCCT TATGAGCATG CCTGTGTTGG GTTGACAGTG	240
GGGGTAATAA TGACTTGTG GTTGATTGTA GATATTGGGC TGTTAATTGT CAGTTCACTG	300
TTTTAATCTG ACCCAGGCTT ATGCAGGAGGA GAATGTTTC ATGTTACTTA TACTAACATT	360
AGTTCTCTA TAGGGTGATA GATTGGTCCA ATTGGGTGTG AGGAGTTCAAG TTATATGTTT	420
GGGATTTTT AGGTAGTGGG TGTTGANCTT GAACGCTTTC TTAATTGGTG GCTGCTTTA	480
RGCCTACTAT GGGTGGTAAA TGGC	505

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TAGACTGACT CATGTCCCC ACCAAAGCCC ATGTAAGGAG CTGAGTTCTT AAAGACTGAA	60
GACAGACTAT TCTCTGGAGA AAAATAAAAT GGAAATTGTA CTTTAAAAAA AAAAAAAATC	120
GGCCGGGCAT GGTAGCACAC ACCTGTAATC CCAGCTACTA GGGGACATGA GTCAGTCTA	179

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

AGACTGACTC ATGTCCCCTA	CCCCACCTTC	TGCTGTGCTG	CCGTGTTCCCT	AACAGGTCAC	60
AGACTGGTAC TGGTCAGTGG	CCTGGGGGTT	GGGGACCTCT	ATTATATGGG	ATACAAATTT	120
AGGAGTTGGA ATTGACACGA	TTTAGTGACT	GATGGGATAT	GGGTGGTAAA	TGGCTA	176

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGACTGACTC ATGTCCCCTA	TTTAACAGGG	TCTCTAGTGC	TGTGAAAAAA	AAAAATGCTG	60
AACATTGCAT ATAACTTATA	TTGTAAGAAA	TACTGTACAA	TGACTTTATT	GCATCTGGGT	120
AGCTGTAAGG CATGAAGGAT	GCCAAGAAGT	TTAAGGAATA	TGGGTGGTAA	ATGGCTAGGG	180
GACATGAGTC AGTCTA					196

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GACGCTTGGC CACTTGACAC	CTTTTATTTT	TTAAGGATTTC	TTAAGTCATT	TANGTNACTT	60
TGTAAGTTTT	TCCTGTGCC	CCATAAGAAT	GATAGCTTTA	AAAATTATGC	120
AAGAAGATAC	TTCTAGCTTT	AGAATGTGTA	GGTATAGCCA	GGATTCTTGT	180
GATTTAGAGC	AAATTTCTTA	TTCTCCTTGC	CTCATCTGTA	ACATGGGGAT	240
CTGGCTTGAC	AAGGTTGGAA	TTAGTATTAC	ATGGTAAATA	CATGAAAAT	300
GTGCCAAGTA	TCTAGGAAGT	ACTTGGGCAT	GGGTGGTAAA	TGGCT	345

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GACGCTTGGC CACTTGACAC TAGAGTAGGG TTTGGCCAAC TTTTCTATA AAGGACCAGA	60
GAGTAAATAT TTCAGGCTT GTGGGTTGTG CAGTCTCT TGCAACTACT CAGCTCTGCC	120
ATTGTAGCAT AGAAATCAGC CATAGACAGG ACAGAAATGA ATGGGTGGTA AATGGCTA	178

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

TGGGCACCTT CAATATCTAT CCAGCGCATC TAAATTGCT TTTTCTTGA TTAAAAATT	60
CACCACTTGC TGTGTTTGCT CATGTATACC AAGTAGCAGT GGTGTGAGGC CATGCTTGT	120
TTTGATTG ATATCAGCAC CGTATAAGAG CAGTGTCTTG GCCATTAATT TATCTTCATT	180
GTAGACAGCA TAGTGTAGAG TGGTATCTCC ATACTCATCT GGAATATTTG GATCAGTGCC	240
ATGTTCCAGC AACATTAACG CACATTATC TTCCTGGCAT TGTACGGCCT TTGTCAGAGC	300
TGTCCTCTT TTGTTGTCAA GGACATTAAG TTGACATCGT CTGTCAGAGCA CGAGTTTAC	360
TACTTCTGAA TTCCCATTGG CAGAGGCCAG ATGTAGAGCA GTCCTCTTT GCTTGTCCCT	420
CTTGTTCACA TCAGTGTCCC TGAGCATAAC GGAA	454

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

TCCGTTATGC CACCCAGAAA ACCTACTGGA GTTACTTATT AACATCAAGG CTGGAACCTA	60
TTTGCTCAG TCCTATCTGA TTCATGAGCA CATGGTTATT ACTGATCGCA TTGAAAACAT	120
TGATCACCTG GGGTTCTTA TTTATCGACT GTGTGATGAC AAGGAAACTT ACAAACTGCA	180
ACGCAGAGAA ACTATTAAAG GTATTGAGAA ACGTGAAGCC AGCAATTGTT TCGCAATTG	240
GCATTTGAA AACAAATTG CCGTGAACAC TTTAATTGT TCTTGAACAG TCAAGAAAAA	300
CATTATTGAG GAAAATTAAAT ATCACAGCAT AACGGAA	337

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

TCGGGTGATG CCTCCTCAGG CATCTCCAT CCATCTCTC AAGATTAGCT GTCCCAAATG	60
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TTTTCCCTTC TCTTCTTTAC TGATAAAATTG GGACTCCTTC TTGACACTGA TGACAGCTT	120
AGTATCCTTC TTGTCACCTT GCAGACTTTA AACATAAAAAA TACTCATTGG TTTTAAAAGG	180
AAAAAGTAT ACATTAGCAC TATTAAGCTT GCCCTTGAAA CATTCTAT CTTTTATTAA	240
ATGTCGGTTA GCTGAACAGA ATTCACTTTA CAATGCAGAG TGAGAAAAGA AGGGAGCTAT	300
ATGCATTGA GAATGCAAGC ATTGTCAAAT AAACATTTA AATGCTTCT TAAAGTGAGC	360
ACATACAGAA ATACATTAAG ATATTAGAAA GTGTTTTGC TTGTGTACTA CTAATTAGGG	420
AAGCACCTTG TATAGTCCT CTTCTAAAAT TGAAGTAGAT TTTAAAACC CATGTAATT	480
AATTGAGCTC TCAGTTCAGA TTTTAGGAGA ATTTAACAG GGATTGGTT TTGTCTAAAT	540
TTTGTCAATT TNTTGTAGTTA ATCTGTATAA TTTTATAAAT GTCAAACGTG ATTTAGTCCG	600
TTTCATGCT GCTATGAAAG AAATACCCAN GACAGGGTTA TTTATAAANG GAAAGANGTT	660
AATTGACTC CCAGTTACACA GGCCCTGAGGA NGNATCNCCC GAAATCCTTA TTGCG	715

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

GGTAANGNGC ATACNTCGGT GCTCCGGCCG CCGGAGTCGG GGGATTCGGG TGATGCCTCC	60
TCAGGCCAC TTGGCCCTGC TTTTCCAAA TGGCAGCTCC TCTGGACATG CCATTCCTTC	120
TCCCACCTGC CTGATTCTTC ATATGTTGGG TGTCCCTGTT TTTCTGGTGC TATTTCCCTGA	180
CTGCTGTTCA GCTGCCACTG TCCTGCAAAG CCTGCCTTT TAAATGCCTC ACCATTCCCT	240
CATTTGTTTC TTAAATATGG GAAGTGAAAG TGCCACCTGA GGCCGGGCAC AGTGGCTCAC	300
GCCTGTAATC CCAGCACTTT GGGAGCCTGA GGAGGCATCA CCCGA	345

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GGTGATGCCT CCTCAGGGCA AGCTCAGGGG GGACAGAAAC CTCCCGTGA GCAGAAGGGC	60
AAAAGCTCGC TTGATCTTGA TTTTCAGTAC GAATACAGAC CGTGAAAGCG GGGCCTCACG	120
ATCCTTCTGA CCTTTTGGGT TTTAACGAGG AGGTGTCAGA AAAGTTACCA CAGGGATAAC	180
TGGCTTGTGG CGGCCAAGCG TTCATAGCGA CGTCGCTTT TGATCCTTCG ATGTCGGCTC	240
TTCCTATCAT TGTGAAGCAG AATTCAACAA GCGTTGGATT GTTCACCCAC TAATAGGGAA	300
CGTGAGCTGG GTTTAGACCG TCGTGAGACA GGTTAGTTT ACCCTACTGA TGATGTGKG	360
TTGCCATGGT AATCCTGCTC AGTACGAGAG GAACCGCAGG TTCASACATT TGGTGTATGT	420
GCTTGCCTT	429

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TGACACCTAT	GTCCNGCATC	TGTTCACAGT	TTCCACAAAT	AGCCAGCCTT	TGGCCACCTC	60
TCTGTCTGA	GGTATAACAAG	TATATCAGGA	GGTGTATAACC	TTCTCTTCTC	TTCCCCCACCA	120
AAGAGAACAT	GCAGGGCTCTG	GAAGCTGTCT	TAGGAGCCTT	TGGGCTCAGA	ATTCAGAGT	180
CTTGGGTACC	TTGGATGTGG	TCTGGAAGGA	GAAACATTGG	CTCTGGATAA	GGAGTACAGC	240
CGGAGGAGGG	TCACAGAGCC	CTCAGCTCAA	GCCCCGTGTC	CTTAGTCTAA	AAGCAGCTTT	300
GGATGAGGAA	GCAGGGTTAAC	TAACATACGT	AAGCGTACAC	AGGTAGAAAG	TGCTGGGAGT	360
CAGAATTGCA	CACTGTGTAG	GAGTAGTACC	TCAATCAATG	AGGGCAAATC	AACTGAAAGA	420
AGAAGACCNA	TTAATGAATT	GCTTANGGGG	AAGGATCAAG	GCTATCATGG	AGATCTTCT	480
AGGAAGAGATTA	TTGTTTANAA	TTATGAAAGG	ANTAGGGCAG	GGACAGGGCC	AGAAGTANAA	540
GANAACATTG	CCTATANCCC	TTGTCTTGCA	CCCAGATGCT	GGACAAGGTG	TCA	593

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

TGACACCTTG	TCCAGCATCT	GACGTGAAGA	TGAGCAGCTC	AGAGGAGGTG	TCCTGGATTT	60
CCTGGTTCTG	TGGGCTCCGT	GGCAATGAAT	TCTTCTGTGA	AGTGGATGAA	GACTACATCC	120
AGGACAAATT	TAATCTTA	GGACTCAATG	AGCAGGTCCC	TCACTATCGA	CAAGCTCTAG	180
ACATGATCTT	GGACCTGGAG	CCTGATGAAG	AACTGGAAGA	CAACCCCAAC	CAGAGTGACC	240
TGATTGAGCA	GGCAGCCGAG	ATGCTTTATG	GATTGATCCA	CGCCCGCTAC	ATCCTTACCA	300
ACCGTGGCAT	CGCCCAGATG	CTGGACAAGG	TGTCA			335

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

TACGTACTGG	TCTTGAAGGT	CTTAGGTAGA	GAAAAAATGT	GAATATTTAA	TCAAAGACTA	60
TGTATGAAAT	GGGACTGTAA	GTACAGAGGG	AAGGGTGGCC	CTTATGCCA	GAAGTTGGTA	120
GATGCGTCCC	CGTCATGAAA	TGTTGTGTCA	CTGCCCGACA	TTTGCCGAAT	TACTGAAATT	180
CCGTAGAATT	AGTGCAAATT	CTAACGTTGT	TCATCTAAGA	TTATGGTCC	ATGTTCTAG	240
TACTTTTA						248

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TGACGCTTGG CCACTTGACA CAAGTAGGGG ATAAGGACAA AGACCCATNA GGTGGCCTGT	60
CAGCCTTTG TTACTGTTGC TTCCCTGTCA CCACGGCCCC CTCTGTAGGG GTGTGCTGTG	120
CTCTGTGGAC ATTGGTGCAT TTTCACACAT ACCATTCTCT TTCTGCTTCA CAGCAGTCCT	180
GAGGGGGGAG CACACAGGAC TACCTGTCA GATGANGATA ATGATGTCTG GCCAACTCAC	240
CCCCCAACCT TCTCACTAGT TATANGAAGA GCCANGCTA NAACCTTCTA TCCTGNCCCC	300
TTGCCCTATG ACCTCATCCC TGTTCCATGC CCTATTCTGA TTTCTGGTGA ACTTTGGAGC	360
AGCCTGGTTT NTCCCTCCTCA CTCCAGCCTC TCTCCATACC ATGGTANGGG GGTGCTGTT	420
CACNCAAANG GTCAGGTGTG TCTGGGAAT CCTNANANCT GCCNNGAGTT TCCNANGCAT	480
TCTTAAAAAC CTTCTTGCT AATCANATNG TGTCCAGTGG CCAACCNTCN	530

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

TGACGCTTGG CCACTTGACA CTAAATAGCA TCTTCTAAAG GCCTGATTCA GAGTTGTGGA	60
AAATTCTCCC AGTGTCAAGGG ATTGTCAAGGA ACAGGGCTGC TCCTGTGCTC ACTTTACCTG	120
CTGTGTTCT GCTGGAAAAG GAGGGAAAGAG GAATGGCTGA TTTTTACCTA ATGTCTCCCA	180
GTTTTTCATA TTCTTCTTGG ATCCTCTTCT CTGACAACTG TTCCCTTTG GTCTTCTTCT	240
TCTTGCTCAG AGAGCAGGTC TCTTAAAC TGAGAAGGGA GAATGAGCAA ATGATTAAAG	300
AAAACACACT TCTGAGGCC AGAGATCAAA TATTAGGTAA ATACTAAACC GCTTGCTG	360
TGTGGTCACT TTTCTCCTCT TTCACATGCT CTATCCCTCT ATCCCCCACC TATTCATATG	420
GCTTTATCT GCCAAGTTAT CCGGCCTCTC ATCAACCTTC TCCCCTAGCC TACTGGGGGA	480
TATCCATCTG GGTCTGTCTC TGGTGTATTG GTGTCAAGTG GCCAAGCGTC A	531

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ATTGACGCTT GGCCACCTGAC CACCCGCCTG CCTGCAATAC TGGGGCAAGG GCCTTCAGT	60
CTTTCCCTGCC ACCAGCTGCC ACTGCACACA GAGATCAGAA ATGCTACCAA CCAAGACTGT	120
TGGTCCTCAG CCTCTCTGAG GAGAAAGAGC AGAAGCCTGG AAGTCAGAAG AGAAGCTAGA	180
TCGGCTACGG CCTTGGCAGC CAGCTCCCC ACCTGTGGCA ATAAAGTCGT GCATGGCTTA	240
ACAATGGGGG CACCTCCTGA GAAACACATT GTTAGGCAAT TCGGCGTGTG TTCATCAGAG	300

CATATTTACA CAAACCTCGA TAGTGCAGCC TACTATCCAC TATTGCTCCT ACGCTGCAA	360
CCTGAACAGC ATGGGACTGT ACTGAATACT GGAAGCAGCT GGTGATGGTA CTTATTGTTG	420
TATCTAAACA CAGAGAAGGT ACAGTAAGAA TATGGTATCA TAAACTTACA GGGACCGCCA	480
TCCTATATGC AGTCTGTTGT GACCAAAATG TGTCAAGTGG CCAAGCGTCA	530

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

TGTATCGACG TAGTGGTCTC CGGGCTACTA GGCGCGTTGTG TGCTGGTAGT ACCTGGTTCA	60
CTGAAAGGCG CATCTCCCTC CCCCGCGTCGC CCTGAAGCAG GGGGAGGACT TCGCCCAGCC	120
AAGGCAGTTG TATGAGTTT AGCTGCGGCA CTTCGAGACC TCTGAGGCCA CCTCCTTCAG	180
GAGCCTTCCC CGATTAAGGA AGCCAGGGTA AGGATTCCCTT CCTCCCCCAG ACACCACGAA	240
CAAACCCACCA CCCCCCCTAT TCTGGCAGCC CATATACATC AGAACGAAAC AAAAATAACA	300
AATAAACNAA ACCAAAAAAA AAAAGAGAAG GGGAAATGTA TATGTCTGTC CATCCTGTTG	360
CTTTAGCCTG TCAGCTCCTA NAGGGCAGGG ACCGTGTCTT CCGAATGGTC TGTGCAGCGC	420
CGACTGCGGG AAGTATCGGA GGAGGAAGCA GAGTCAGCAG AAGTTGAACG GTGGGCCCGG	480
CGGCTCTTGG GGGCTGGTGT TGTACTTCGA GACCGCTTTC GCTTTTGTC TTAGATTAC	540
GTTTGCTCTT TGGAGTGGGA NACCACTACN TCNATACA	578

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

TGTATCGACG TAGTGGTCTC CTCTTGCAAA GGACTGGCTG GTGAATGGTT TCCCTGAATT	60
ATGGACTTAC CCTAAACATA TCTTATCATC ATTACCAGTT GCAAAATATT AGAATGTGTT	120
GTCACTGTTT CATTGATTCT CTAGAAGGTT AGTCTTAGAT ATGTTACTTT AACCTGTATG	180
CTGTAGTGCT TTGAATGCAT TTTTTGTTTG CATTGTTGTT TGCCCAACCT GTCAATTATA	240
GCTGCTTAGG TCTGGACTGT CCTGGATAAA GCTGTTAAAA TATTCACCAG TCCAGCCATC	300
TTACAAGCTA ATTAAGTCAA CTAAATGCTT CTTGTTTTG CCAGACTTGT TATGTCAATC	360
CTCAATTCTT GGGTTCAATT TGGGTGCCCT AAATCTTAGG GTGTGACTTT CTTAGCATCC	420
TGTAACATCC ATTCCCCAAGC AAGCACAAC TACACATAATA CTTTCCAGAA GTTCATTGCT	480
GAAGCCTTTC CTTCACCCAG CGGAGCAACT TGATTTCTA CAACTTCCCT CATCAGAGCC	540
ACAAGAGTAT GGGATATGGA GACCACTACG TCGATACA	578

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TGTATCGACG TANTGGTCTC CCAAGGTGCT GGGATTGCAG GCATGAGCCA CCACTCCCAG	60
GTGGATCTTT TTCTTTATAC TTACTTCATT AGGTTTCTGT TATTCAAGAA GTGTAGGGT	120
AAAAGTCTTT TCAATCTACA TGGTTAAATA ATGATAGCCT GGGAAATAAA TAGAAATTT	180
TTCTTTCATC TTTAGGTTGA ATAAAGAAC AGAAAAAATA GAACATACTG AAAATAATCT	240
AAGTTCCAAC CATAGAAGAA CTGCAGAAGA AATGAAGAAA GTGATGATGA TTTAGATTT	300
GATATTGATT TAGAAGACAC AGGAGGAGAC CACTACGTCG ATACA	345

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

TGTATCGACG TAGTGGTCTC CAAACTGAGG TATGTGTGCC ACTAGCACAC AAAGCCTTCC	60
AACAGGGACG CAGGCACAGG CAGTTAAAG GGAATCTGTT TCTAAATTAA TTTCCACCTT	120
CTCTAAAGTAT TCTTCTCTAA AACTGATCAA GGTGTGAAGC CTGTGCTCTT TCCCAACTCC	180
CCTTGACAA CAGCCTTCAA CTAACACAAG AAAAGGCATG TCTGACACTC TTCCTGAGTC	240
TGACTCTGAT ACGTTGTTCT GATGCTCTAA GAGCTCCAGA ACACCAAAGG GACAATTCA	300
AATGCTGGTG TATAACAGAC TCCAATGGAG ACCACTACGT CGATACA	347

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

AGGNNGNGGA NTGTATCGAC GTAGTGGTCT CCCAACAGTC TGTCAATTCAAG TCTGCAGGTG	60
TCAGTGTGTTT GGACAATGAG GCACCATTGT CACTTATTGA CTCCTCAGCT CTAAATGCTG	120
AAATTAATC TTGTCATGAC AAGTCTGGAA TTCCTGATGA GGTTTACAA AGTATTGG	180
ATCAATACTC CAACAAATCA GAAAGCCAGA AAGAGGATCC TTTCAATATT GCAGAACAC	240
GAGTGGATTG ACACACCTCA GGAGACCACT ACGTCGATAC A	281

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GGGAAACACT TCCTCCCAGC CTTGTAAGGG TTGGAGCCCT CTCCAGTATA TGCTGCAGAA	60
TTTTTCTCTC GGTTTCTCAG AGGATTATGG AGTCCGCCTT AAAAAGGCA AGCTCTGGAC	120
ACTCTGAAA GTAGAATGGC CAAAGTTGG AGTTGAGTGG CCCCTTGAAG GGTCACTGAA	180

CCTCACAAATT	GTTCAAGCTG	TGTGGCGGGT	TGTTACTGAA	ACTCCCCGCC	TCCCTGATCA	240
GTTTCCCTAC	ATTGATCAAT	GGCTGAGTTT	GGTCAGGAGC	ACCCCTTCCG	TGGCTCCACT	300
CATGCAACCAT	TCATAATTTC	ACCTCCAAGG	TCCCTCTGAG	CCAGACCGTG	TTTCGCCTC	360
GACCCCTCAGC	CGGTTCGGCT	CGCCCTGTAC	TGCCTCTCTC	TGAAGAAGAG	GAGAGTCTCC	420
CTCACCCAGT	CCCACCGCCT	TAAAACCAGC	CTACTCCCTT	AGGGTCATCC	CATGTCTCCT	480
CGGCTATGTC	CCCTGTAGGC	TCATCACCCA	TTGCCTCTTG	GTTGCAACCG	TGGTGGGAGG	540
AAGTAGCCCC	TCTACTACCA	CTGAGAGAGG	CACAAGTCCC	TCTGGGTGAT	GAGTGCTCCA	600
CCCCCTTCCT	GGTTTATGTC	CCTTCTTTCT	ACTTCTGACT	TGTATAATTG	GAAAACCCAT	660
AATCCTCCCT	TCTCTGAAAA	GCCCCAGGCT	TTGACCTCAC	TGATGGAGTC	TGTACTCTGG	720
ACACATTGGC	CCACCTGGGA	TGACTGTCAA	CAGCTCCCTT	TGACCCCTTT	CACCTCTGAA	780
GAGAGGGAAA	GTATCCAAG	AGAGGCCAAA	AAGTACAACC	TCACATCAAC	CAATAGGCCG	840
GAGGAGGAAG	CTAGAGGAAT	AGTGATTAGA	GACCCAAATTG	GGACCTAATT	GGGACCCAAA	900
TTTCTCAAGT	GGAGGGAGAA	CTTTGACGA	TTTCCACCGG	TATCTCCTCG	TGGGTATTCA	960
GGGAGCTGCT	CAGAAACCTA	TAAAATTGTC	TAAGGGCACT	GAAGTCGTCC	AGGGGCATGA	1020
TGAGTCACCA	GGAGTGTGTTT	TAGAGCACCT	CCAGGGAGGCT	TATCAGATT	ACACCCCTTT	1080
TGACCTGGCA	GCCCCCGAAA	ATAGCCATGC	TCTTAATTG	GCATTGTGG	CTCAGGCAGC	1140
CCCAGATAGT	AAAGGAAAC	TCCAAAACT	AGAGGGATT	TGCTGGAATG	AATACCAAGTC	1200
AGCTTTAGA	GATAGCCTAA	AAGGTTTTTG	ACAGTCAAGA	GGTTGAAAAA	CAAAACAAAG	1260
CAGCTCAGGC	AGCTGAAAAA	AGCCACTGAT	AAAGCATCCT	GGAGTATCAG	AGTTTACTGT	1320
TAGATCAGCC	TCATTTGACT	TCCCCTCCCA	CATGGTGT	AAATCCAGCT	ACACTACTTC	1380
CTGACTCAAA	CTCCACTATT	CCTGTTCATG	ACTGTCAAGG	ACTGTTGGAA	ACTACTGAAA	1440
CTGGCCGACC	TGATCTTCAA	AATGTGCCCC	TAGGAAAGGT	GGATGCCACC	ATGTTCACAG	1500
ACAGTAGCAG	CTTCCTCGAG	AAGGGACTAC	GAAAGGCCGG	TGCACTGTT	ACCATGGAGA	1560
CAGATGTGTT	GTGGGCTCAG	GCTTTACAG	CAAACACCTC	AGCACAAAAG	GCTGAATTGA	1620
TCGCCCTCAC	TCAGGCTCTC	CGATGGGGTA	AGGATATTAA	CGTTAACACT	GACAGCAGGT	1680
ACGCCTTGC	TACTGTGCAT	GTACGTGGAG	CCATCTACCA	GGAGCGTGGG	CTACTCACCT	1740
CAGCAGGTGG	CTGTAATCCA	CTGTTAAAGGA	CATCAAAAGG	AAAACACGGC	TGTTGCCGT	1800
GGTAACCAGA	AGCTGATTTC	AGCAGCTCAA	GATGCAGTGT	GACTTCAGT	CACGCCTCTA	1860
AACTTGCTGC	CCACAGTCTC	CTTTCCACAG	CCAGATCTGC	CTGACAATCC	CGCATACTCA	1920
ACAGAAGAAG	AAAACGGCC	TCAGAACTCA	GAGCCAATAA	AAATCAGGAA	GGTTGGTGGA	1980
TTCTTCTGA	CTCTAGAAC	TTCATACCCC	GAACCTCTGG	GAAAACCTTA	ATCAGTCACC	2040
TACAGTCTAC	CACCCATTAA	GGAGGAGCAA	AGCTACCTCA	GCTCCTCCGG	AGCCGTTTTA	2100
AGATCCCCCA	TCTTCAAAGC	CTAACAGATC	AAGCAGCTCT	CCGGTGCACA	ACCTGCGCCC	2160
AGGTAAATGC	CAAAAAAGGT	CCTAAACCCA	GCCCAGGCCA	CCGTCTCCAA	GAAAACTCAC	2220
CAGGAGAAAA	GTGGGAAATT	GACTTTACAG	AAGTAAAACC	ACACCGGGCT	GGGTACAAAT	2280
ACCTTCTAGT	ACTGGTAGAC	ACCTCTCTG	GATGGACTGA	AGCATTGCT	ACCAAAAACG	2340
AAACTGTCAA	TATGGTAGTT	AAGTTTTAC	TCAATGAAAT	CATCCCTCGA	CATGGGCTGC	2400
CTGTTGCCA	TAAGGGTCTGA	TAATGGACCG	GCCTTCGCCT	TGTCTATAGT	TTAGTCAGTC	2460
AGTAAGGCGT	TAACACATTCA	ATGGAAGCTC	CATTGTGCCT	ATCGACCCCA	GAGCTCTGGG	2520
CAAGTAGAAC	GCATGAAC	CACCTAAAAA	AAACACTCTA	CAAATTAAT	CTTAGAAACC	2580
GGTGTAAATT	GTGTAAGTCT	CCTTCCTTAA	GCCCTACTTA	GAGTAAGGTG	CACCCCTTAC	2640
TGGGCTGGGT	TCTTACCTTT	TGAAATCATG	TATGGGAGGG	TGCTGCCTAT	CTTGCTTAAG	2700
CTAAGAGATG	CCCAATTGGC	AAAATATCA	CAAACATTAATT	TATTACAGTA	CCTACAGTCT	2760
CCCCAACAGG	TACAAGATAT	CATCTGCCA	CTTGTTCGAG	GAACCCATCC	CAATCCAATT	2820
CCTGAACAGA	CAGGGCCCTG	CCATTCATTC	CCGCCAGGTG	ACCTGTTGTT	TGTTAAAAG	2880
TTCCAGAGAG	AAGGACTCCC	TCCTGCTTGG	AAGAGACCTC	ACACCGTCAT	CACGATGCCA	2940
ACGGCTCTGA	AGGTGGATGG	CATTCTGCG	TGGATTTCATC	ACTCCGCAT	CAAAAAGGCC	3000
AACAGAGCCC	AACTAGAAAC	ATGGGTCCCC	AGGGCTGGGT	CAGGCCCTT	AAAACGTGAC	3060
CTAAGTTGGG	TGAAGCCATT	AGATTAATT	TTTTCTTAA	TTTTGTAAAA	CAATGCATAG	3120
CTTCTGTCAA	ACTTATGTAT	CTTAAGACTC	AATATAACCC	CCTGTTATA	ACTGAGGAAT	3180
CAATGATTG	ATTCCCCAA	AAACACAAGT	GGGGAATGTA	GTGTCCAACC	TGGTTTTAC	3240
TAACCCGTGTT	TTAGACTCT	CCCTTCCCTT	TAATCACTCA	GCTTGTTC	ACCTGAATTG	3300
ACTCTCCCTT	AGCTAAGAGC	GCCAGATGGA	CTCCATCTG	GCTCTTTCAC	TGGCAGCCGC	3360
TTCCTCAAGG	ACTTAAC	TGCAAGCTGA	CTCCCAGCAC	ATCCAAGAAT	GCAATTAAC	3420
GATAAGATA	TGTGGCAAGC	TATATCCGCA	GTTCCCAGGA	ATTGTC	CACAG	3480

CCCTCTTACC	CTTCAGCAAC	CACCACCTG	ATCAGTCAGC	AGCCATCAGC	ACCGAGGCAA	3540
GGCCCTCCAC	CAGAAAAAG	ATTCTGACTC	ACTGAAGACT	TGGATGATCA	TTAGTATTTT	3600
TAGCAGTAA	TTTTTTTTT	CTTTTCTT	CTTTTTCT	CGTGC		3646

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

TAAGAGGGTA	CAAGATCTAA	GCACAGCCGT	CAATGCAGAA	CACAGAACGT	AGCCTGGTAA	60
GTGTGTTAAG	AGTGGGAATT	TTTGGAGTAC	AGAGTAAGGC	ACCTAACCT	AGCTGGGTT	120
TGGTGACGGT	CCCAAGATGGC	TTACAGAAGA	AAAGTGTCTG	AGATGAGTTT	TTAAGAATGA	180
ATAAGGATAG	ACACAAGTGA	GGACTGACTT	GGCAGTGGTG	AATGGTGGGT	GGCAAAAAAC	240
TTCGCATGTA	TGGAAACTGC	ACGTACAGGA	ATGAAGAATG	AGACTGTGTG	GTGTTAATG	300
AGCTGCAAAT	ACTAATTTA	TCCTGAAAGT	TTTGAAGAGT	TAACTAAAAA	GTATTTTTA	360
GTAAGGAAAT	AACCCTACAT	TTCAGGGTTA	TTGTTGTTT	ANATATTGAA	GGTGCCAA	419

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

AAGAGGGTAC	CTGTATGTAG	CCATGGTGGC	AATGAGAGAC	TGATTACTAC	CTGCTGGAGA	60
TTGTTTAAGT	GAGTTAATAT	ATTAAGGATA	AAGGGAGCCA	GGTTTTTGA	CTGTTGGAGA	120
AGGAAATTAC	AGATATTGAA					148

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

TAAGAGGGTA CMAAAAAAA AAAATAGAAC GAATGAGTAA GACCTACTAT TTGATAGTAC	60
AACAGGGTGA CTATAGTCAA TGATAACTTA ATTATACATT TAACATAGAG TGTAATTGGA	120
TTGTTGTAA CTCGAAGGAT AAATGCTTGA GAGGATGGAT ACCCCATTCT CCATGATGTA	180
CTTATTCAC ATTACATGCC TGTATCAAAG CATCTCATAT ACCCTATAAA TATGTACACC	240
TACTATGTAC CCTCTTA	257

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

TAAGAGGGTA CGGGTATTG CTGATGGGAT TTTTTTTCT TTCTTTTCT TTGGAAAACA	60
AAATGAAAGC CAGAACAAA TTATTGAACA AAAGACAGGG ACTAAATCTG GAGAAATGAA	120
GTCCCCTCAC CTGACTGCCA TTTCATTCTA TCTGACCTTC CAGCTAGGT TAGGAGAATA	180
GGGGGTGGAG GGGATTAATC TGATACAGGT ATATTTAAAG CAACTCTGCA TGTGTGCCAG	240
AAGTCCATGG TACCCCTCTTA	260

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

TGCTCCTCTT GCCTTACCAA CCACAAATTA GAACCATAAT GAGATGTCAC CTCATACCTG	60
GTGGGATTAA CATTATTTAA AAAATCAGAA GTATTGACAA GGATGTGAAG AAATTAGAAC	120
ATCTGTGAC TGTGGTGGG AATGTAAAAA AGGTGTGGCC ACTATGGTA ACAGCATGAA	180
GGTCCTCAA AAAAATTTT TTTAACCTA CTCTATGATC GATCTTGAGG TTGTTTATGC	240
AAAAGAAC TG AAATCAGGAT TTTGAGGAAA TATTACATT CCCACATCCA TTTCTGCTT	300
ATTCAATAA CTCAAGAGAT GGAAACAACC TAAATGTCCA TCCCGGGATG AATGGATAAA	360
CACAGTGTGG TATATGCATA CAATGGAATA TTATTTAGTC TTTAAAAAGA AAAATTCTAT	420

CATATACTAC AACTTANATN AACCTTGAGG ACACAATGCT NAGTGAAATA AGCCACGGAA	480
GGACGAATAAC TGCATTATTC CCTTATATGA AGTATCTAAA GTGGTCAAAC TCTTANAGCA	540
NAAAGTAAAA ATGGGTGGTT GCCANACAGT TGGTTAGGCN AGAAGANAAN CCTANT	596

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

TCTTCTGAAG ACCTTTCGCG ACTCTTAAGC TCGTGGTTGG TAAGGCAAGA GGAGCGTTGG	60
TAAGGCAAGA GGAGCGTTGG TAAGGCAAGA GGAGCA	96

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

TGTAAGTCGA GCAGTGTGAT GATAAAACTT GAATGGATCA ATAGTTGCTT CTTATGGATG	60
AGCAAAGAAA GTAGTTCTT GTGATGGAAT CTGCTCCTGG CAAAAATGCT GTGAACGTTG	120
TTGAAAAGAC AACAAAGAGT TTAGAGTAGT ACATAAATTG AGAATAGTAC ATAAACTTAG	180
AATAGTACAT AAACTTAGTA CATAAATAAT GCACGAAGCA GGGGCAGGGC TTGAGAGAAT	240
TGACTTCAAT TTGGAAAGAG TATCTACTGT AGGTTAGATG CTCTCAAACA GCATCACACT	300
GCTCGACTTA CAA	313

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

AACGAGGACA GATCCTAAA AAGAATGTTG AGTAAAAAAA GTAGAAAATA AGATAATCTC	60
CAAAGTCCAG TAGCATTATT TAAACATTTT TAAAAAAATAC ACTGATAAAA ATTTTGTACA	120
TTTCCCAAAA ATACATATGG AAGCACAGCA GCATGAATGC CTATGGGRTT GAGGATAGGG	180
GTTGGGAGTA GGGATGGGGA TAAAGGGGGA AAATAAAACC AGAGAGGAGT CTTACACATT	240
TCATGAACCA AGGAGTATAA TTATTTCAAC TATTTGTACC WGAAGTCCAG AAAGAGTGGA	300
GGCAGAAGGG GGAGAAGAGG GCGAAGAAC GTTTTGGA GAGGGGTCCC ASAAGAGAGA	360
TTTTCGCGAT GTGGCGCTAC ATACGTTTT CCAGGATGCC TTAAGCTCTG CACCCTATTT	420
TTCTCATCAC TAATATTAGA TTAAACCCCTT TGAAGACAGC GTCTGTGGTT TCTCTACTTC	480
AGCTTCCCT CCGTGTCTTG CACACAGTAG CTGTTTACA AGGGTTGAAC TGACTGAAGT	540
GAGATTATTG	550

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

TAGACTGACT CATGTCCCCT ACCAGAGTAG CTAGAATTAA TAGCACAAAGC CTCTACACCC	60
AGGAACTCAC TATTGAATAC ATAAATGGAA TTTATTCAAG CTTAAAAAGT TTGGAAGGAA	120
ATTCTGACAT ATGCTAAAAC ATGGATGAAC CTTGAAGACT TTATGATAAG TAAAAGAAC	180
CAGTCATAAA AGGAAAAATA TTGCATGATT CCACTTATAT GAGGTACCTA GAGTAGTCAA	240
TTTCATAGAA ACACAAAATA GAATGGTGTGTT TGCCAGGGCT TTTGAGGAAA AGGAAATGAC	300
AAGTTAGGGG ACATGAGTCA GTCTA	325

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

TAGACTGACT CATGTCCCCT ATCTACTCAA CATTTCACACT TGAAGTCTGA TAGGCATCTC	60
AGACTTATCT TGTCCCAAAG CAAACTCTTT ATTTCTTTTC ATCCTAGTCT TTATTTCTTG	120
TGCTGTCTTA CCCATCTCAA AAGAGTGCCA AAATCCACCA AGTTGCTGAA ACAGAAATCT	180

AAGAAATATC CTTGATTCTT CTTTTCCCA TCTACTTCAC TTCTAATTCA TTAGTAAATA	240
ATCTGTTCA GAAAACCAAA CACCTCATGT TCTCACTCAT AAGGGGGAGT TGAACAAATGA	300
GAACACACAG ACACAGGGAG GGGAACATCA CACACCACGG CCCGTCAGGG AGTANGGGAC	360
ATGAGTCAGT CTA	373

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

TAGACTGACT CATGTCCCCT ATAATGCTCC CAGGCATCAG AAAGCATCTC AAACTGGAGC	60
TGACACCAG GCAGAGGTTT CAGGTAAGTC ACAAAAGGGG TCCTAAAGAA TTTGCCCTCA	120
ATATCAGAGT GATTAGAAGA AGTGGACAGA GCTACCCAAG TAAACATAT GCGAGATAAA	180
AAAAATATGG CACTTGTGAA CACACACTAC AGGAGGAAAA TAAGGAACAT AATAGCATAT	240
TGTGCTATTG TGATGATGAA GAACCTCTCT ANAAGAAAA ATAACCAAAG AAACAAAGAA	300
AATTCCCTGCN AATGTTAAC GCTATAGAAC AAATTAACAA AAACATATAT TCAATGAATT	360
CAGAAAAGTT AGCAGGTCAN AAGAAAACAA ATCAAAGACC AGAATAATCC CATTAGAT	420
TGTCGAGTAA ACTANAACAG AAAGAATACC ACTGGAAATT GAATTCCCTAC GTANGGGACA	480
TGANTCANTC TA	492

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

TGGAAAGTAT TTAATGATGG GCAACTTGCT GTTTACTTCC TACATATCCC ATCATCTTCT	60
GTATTTTTT AAATAACTTT TTTTTGGATT TTTAAAGTAA CCTTATTCTG AGAGGTAACA	120
TGGATTACAT ACTTCTAACG CATTAGGAGA CTCTATGTTA AACCAAAAGG AAATGTTACT	180
AGATCTTCAT TTGATCAATA GGATGTGATA ATCATCATCT TTCTGCTCTA ATGGAAAAGT	240
ACTANAAACA TGGAACCATATA ATCTTAGATG AACAACGTAA GAATTGACACAA	300
GAATTTCACT AATTGGCAA ATGTGGGCA GTGACACAAAC ATTTCATGAC GGGGACGCAT	360
CTACCAACTT CTGGCGATAA GGGCCACCCCT TCCCTCTGTA CTTACAGTCC CATTTCATAC	420
ACAGTCTTG ATTAATATT CACATTCTT CTCTACCTAA AGACCTTCAA GACCAGTACG	480
TA	482

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 519 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

TGTATCGACG TAGTGGTCTC CCCATGTGAT AGTCTGAAAT ATAGCCTCAT GGGATGAGAG	60
GCTGTGCCCG AGCCCGACAC CCGTAAAGGG TCTGTGCTGA GGTGGATTAG TAAAAGAGGA	120
AAGCCTTGCA GTTGAGATAG AGGAAGGGCA CTGTCTCCTG CCTGCCCCCTG GGAACTGAAT	180
GTCTCGGTAT AAAACCCGAT TGTACATTG TTCAATTCTG AGATAGGAGA AAAACCAAC	240
TATGGCGGGA GGCAGACAT GTTGGCAGCA ATGCTGCCTT GTTATGCTTT ACTCCACAGA	300
TGTTTGGGCG GAGGGAAACA TAAATCTGGC CTACGTGCAC ATCCAGGCAT AGTACCTCCC	360
TTTGACTTA ATTATGACAC AGATTCCCTT GCTCACATGT TTTTTGCTG ACCTTCTCCT	420
TATTATCACC CTGCTCTCCT ACCGCATTCC TTGTGCTGAG ATAATGAAAA TAATATCAAT	480
AAAAACTTGA NGGAACCTCGG AGACCACTAC GTCGATACA	519

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 771 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

TGTATCGACG TAGTGGTCTC CACTCCGCC TTGACGGGGC TGCTATCTGC CTTCCAGGCC	60
ACTGTCACGG CTCCCGGGTA GAAGTCACTT ATGAGACACA CCAGTGTGGC CTTGTTGGCT	120
TGAAGCTCCT CAGAGGAGGG TGGAACAGA GTGACCGAGG GGGCAGCCTT GGGCTGACCT	180
AGGACGGTCA GCTTGGTCCC TCCGCCAAAC ACGAGAGTGC TGCTGTTGT ATATGAGCTG	240
CAGTAATAAT CAGCCTCGTC CTCAGCCTGG AGCCCAGAGA TGTCAGGGA GGCGGTGTTG	300
CCANACTTGG AGCCAGAGAA GCGATTAGAA ACCCTGAGG GCCGATTACC GACCTCATAA	360
ATCATGAATT TGGGGCTTT GCCTGGTGC TGTTGGTACC ANGAGACATT ATTATAACCA	420
CCAACGTCAC TGCTGGTTC ANTGCAGGGA AAATGGTTGA TCNAACTGTC CAAGAAAACC	480
ACTACGTCCA TACCAATCCA CTAATTGCCN GCGCCTGCA GGTTCAACCA TATTGGGAA	540
NAACTCCCCN CCGCCGTTTG GGATTGNCAT NAACCTTGA AATTGTTCC TATTANTTGT	600
CCCCCTAAAA TAAACCNTTG GGCNTTAATC CATTGGGTCC ATANCTTNTT TNCCCGGTTT	660
TTAAAANTTG TTTATCCCGC CNCCCNATT CCCCCCAAC TTTCAAAAC CCGAAACCN	720
TNAAATTNTN TNAAACCTG GGGGTTCCC NNAATTNNAN TTNAANCTNC C	771

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

TGGGCACCTT CAATATCGGG CTCATCGATA ACATCACGCT GCTGATGCTG CTGTTGCTGG	60
TCCTCTCTAG GAACCTCTGG ATTTCAAAT TCTTTGAGGA ATTCACTCAA ATTATCTGCC	120
TCTCCTCCTT TCCTCCTTT TCTAAGGTCT TCTGGTACAA GCGGTCA	167

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

TTGGGCACCT TCAATATCTA CTGATCTAAA TAGTGTGGTT TGAGGCCTCT TGTTCCCTGGC	60
TAAAAATCCT TGGCAAGAGT CAATCTCCAC TTTACAATAG AGGTAAAAAT CTTACAATGG	120
ATATTCTTGA CAAAGCTAGC ATAGAGACAG CAATTTACA CAAGGTATTT TTCACCTGTT	180
TAATAACAGT GGTTCCTCTA CACCCATAGG GTGCCACCAA GGGAGGAGTG CACAGTTGCA	240
GAAACAAATT AAGATACTGA AGACAACACT ACTTACCAATT TCCCGTATAG CTAACCACCA	300
GTTCAACTGT ACATGTATGT TCTTATGGGC AATCAAGA	338

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

TTTTGGCTC CCATACAGCA CACTCTCATG GGAAATGTCT GTTCTAAGGT CAACCCATAA	60
TGCAAAATC ATCAATATAC TTGAAGATCC CCGTGTAGG TACAATGTAT TTAATATTAT	120
CACTGATACA ATTGATCCAA TACCAAGTTT AGTCTGGCAT TGAATCAAAT CACTGTTTT	180
GTTGTATAAA AAGAGAAATA TTTAGCTTAT ATTTAAGTAC CATATTGTAA GAAAAAAAGAT	240
GCTTATCTTT ACATGCTAAA ATCATGATCT GTACATTGGT GCAGTGAATA TTACTGTAAA	300
AGGGAAAGAAG GAATGAAGAC GAGCTAAGGA TATTGAAGGT GCCCAA	346

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

ACCAATCCCC CACGGATACT GAGGGACAAG TATATCATCC CATTTCATCC CTACAGCAGC	60
AACTTCATGA GGCAGGAGTT ATTAGTCCCA TTTTACAGAA GAGGAAACTG AGACTTAGGG	120
AGATCAAGTA ATTTGCCAG GTCGCACAAAT TAGTGTAGA GCCAGGGCTT GAAGCGACGT	180
CTGTCTTAAG CCAATGACCC CTGCAGATTAA TTAGAGCAAC TGTTCTCCAC AACAGTGTAA	240
GCCTCTTGCT ANAAGCTCAG GTCCACAAGG GCAGAGATT TTGTCTGTT TGCTCATTGC	300
TCCTTCCCCA TTGCTTAGAG CAGGGCTGTC CACGAANCAG GTTCTCAATG CATAGTTATT	360
AAATGTATAT AAGAGCAAAAC ATATGTTACA GAGAACTTTC TGTATGCTTG TCACCTACAT	420
GAATCACCTG TGANATGGGT ATGCTTGTTC CCCANTGTG CAGATNAAGA TATTGAANGT	480
GCCCCAAATCA CTANTTGCAG GCGCCTGCAN GTCCANCATA T	521

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

TGGAACCAAT CCAAATACCC ATCAATGATA GACTGGATAA AGAAAATTTG GCACATGTT	60
ACCATGAAAT ACTATGCAGC CATAAAAAG GATGAGTTCA TATCCTTGC AGGGACATGG	120
ATGAAGCTGG AGACCACAT TCTCAGCAAA CTAACAAGGG AACAGAAAAC CAAACACTGC	180
ATGTTCTCAC TCTTAAGTGG GAGCTGAACA ATGAGAACAC ATGGACACAG GGAGGGGAAC	240
ATCACACAGT GGGGCCTGCT GGTGGTAGG GGTCTAGGGG AGGGATAGCA TTAGGAGAAA	300
TACCTAATGT AGATGACGGG TTGATGGTG CAGCAAACCA CCATGACACG TGTATACCTA	360
TGTAACAAAC CTGCATGTT TGCACATGTA CCCCAGAACT TAAAGTGTAA ATAAAAAAAT	420
TAAGAAAAAA GTTAAGTATG TCATAGATAAC ATAAAAATATT GTANATATTG AAGGTGCCA	480

AA

482

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

TTCGATACAG GCACAGAGTA AGCAGAAAAA TGGCTGTGGT TTAACCAAGT GAGTACAGTT	60
AAGTGAGAGA GGGGCAGAGA AGACAAGGGC ATATGCAGGG GGTGATTATA ACAGGTGGTT	120
GTGCTGGAA GTGAGGGTAC TCGGGGATGA GGAACAGTGA AAAAGTGGCA AAAAGTGGTA	180
AGATCAGTGA ATTGTACTTC TCCAGAATTG GATTCTGGN GGAGTCAAAT AACTATCCAG	240
TTTGGGTAT CATANGCAA CAGTGAGGT ATAGGAGGTA GAAGTCNCAG TGGGATAATT	300
GAGGTTATGA ANGGTTTGGT ACTGACTGGT ACTGACAANG TCTGGTTAT GACCATGGGA	360
ATGAATGACT GTANAAGCGT ANAGGATGAA ACTATTCCAC GANAAAGGGG TCCNAAAACT	420
AAAAANNNAA GN>NNNNNGGG AATATTATTT ATGTGGATAT TGAANGTGCC CAAA	474

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

TTCGATACAG GCAAACATGA ACTGCAGGAG GGTGGTGACG ATCATGATGT TGCCGATGGT	60
CCGGATGGNC ACGAAGACGC ACTGGANCAC GTGCTTACGT CCTTTGCTC TGTTGATGGC	120
CCTGAGGGGA CGCAGGACCC TTATGACCCCT CAGAATCTTC ACAACGGGAG ATGGCACTGG	180
ATTGANTCCC ANTGACACCA GAGACACCCC AACCAACAGN ATATCANTAT ATTGATGTAG	240
TTCTGTAGA NGGCCCCCTT GTGGAGGAAA GCTCCATNAG TTGGTCATCT TCAACAGGAT	300
CTAACAGTT TCCGATGGCT GTGATGGCA TAGTCATANT TAACCNTGTN TCGAA	355

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

TTGGATTGGT CCTCCAGGAG AACAAAGGGGA AAAAGGTGAC CGAGGGCTCC CTGGAACCTCA	60
AGGATCTCCA GGAGCAAAAG GGGATGGGG AATTCTGGT CCTGCTGGTC CCTTAGGTCC	120

ACCTGGTCCT CCAGGCTTAC CAGGTCTCA AGGCCAAAG GGTAAACAAAG GCTCTACTGG	180
ACCCGCTGGC CAGAAAGGTG ACAGTGGTCT TCCAGGGCCT CCTGGGCCTC CAGGTCCACC	240
TGGTGAAGTC ATTCAAGCTT TACCAATCTT GTCCTCCAAA AAAACGAGAA GACATACTGA	300
AGGCATGCAA GCAGATGCAG ATGATAATAT TCTTGATTAC TCGGATGGAA TGGAAAGAAAT	360
ATTGGTTCC CTCATTCCC TGAAACAAGA CATCGAGCAT ATGAAATTTC CAATGGGTAC	420
TCAGACCAAT CCAA	434

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

TGGATTGGTC ACATGGCAGA GACAGGATTC CAAGGCAGTG AGAGGGAGGAT ACAATGCTTC	60
TCACTAGTTA TTATTATTTA TTTTATTTTT GAGATGAAGT CTCGCTTTGT CTCCCAGGCT	120
GGAGAGCGGT GGTGCGATCT TGGCTCTCTG CAACCCCCGC CTCAAGCAAT TCTCCTGTCT	180
TAGCCTCGCG GGTAGATGGA ATTACAGGCG CCCACCGCCA TGCCCAACTA ATTTTTTGT	240
GTCTTCAGTA GAGACAGGGT TTGCCCCATGT TGGGCAGGCT GGTCTTGAAC TCCTGACCTC	300
NAGTGATCTG CCCTCCTCGG CCTCACAAAG TGCTGGAATT ACAGGCATGG GCTGCTGCAC	360
CCAGTCACACT TCTCACTAGT TATGGCCTTA TCATTTCAC CACATTCTAT TGGCCCAAAA	420
AAAAAAAAAN	430

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

TGGTACTCCA CCATYATGGG GTCAACCGCC ATCCTCGCCC TCCTCCTGGC TGTTCTCAA	60
GGAGTCTGTG CCGAGGTGCA GCTGRTGCAG TCTGGAGCAG AGGTAAAAA GTCCGGGGAG	120
TCTCTGAAGA TCTCCTGTAA GGGTTCTGGA TACACCTTTA AGATCTACTG GATCGCCTGG	180
GTGCGCCAGT TGCCCCGGAA AGGCCTGGAG TGGATGGGGC TCATCTTCC TGATGACTCT	240
GATACCAGAT ACAGCCCGTC CTTCCAAGGC CAGGTACCCA TCTCAGTCGA TAAGTCCATC	300
AGCACCGCCT ATCTGCAGTG GAGTACCAA	329

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

TGGTACTCCA CTCAGCCAA CCTTAATTAA GAATTAAGAG GGAACCTATT ACTATTCTCC	60
CAGGCTCCTC TGCTCTAACCC AGGCTCTGG GACAGTATTA GAAAAGGATG TCTCAACAAG	120

TATGTAGATC	CTGTACTGGC	CTAAGAAGTT	AAACTGAGAA	TAGCATAAAAT	CAGACCAAAC	180
TTAATGGTCG	TTGAGACTTG	TGTCCTGGAG	CAGCTGGGAT	AGGAAAACCTT	TTGGGCAGCA	240
AGAGGAAGAA	CTGCCTGAA	GGGGCACTCA	TGTTAAAAT	TACAAGGGGA	ACCCACACCA	300
GGCCCCCTTC	CCAGCTCTCA	GCCTAGAGTA	TTAGCATTTC	TCAGCTAGAG	ACTCACAAC	360
TCCTTGCTTA	GAATGTGCCA	CCGGGGGGAG	TCCCTGTGGG	TGATGAGGCT	CTCAAGAGTG	420
AGAGTGGCAT	CCTATCTTCT	GTGTGCCAC	AGGAGCCTGG	CCCGAGACTT	AGCAGGTGAA	480
GTTCCTGGTC	CAGGCTTGC	CCTTGACTCA	CTATGTGACC	TCTGGTGGAG	TACCAA	536

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

NTGTTGCGAT	CCCAGTAAC	CGGGAAAGCTG	AGGCAGGGAGG	ATCACCTGAG	CTCAGGAGGT	60
TGAGGCCGA	GTGAGCCGGG	ACCACGCCAC	TACACTCCAG	CCTGGGGCAT	AGAGTGGAGAC	120
CCTCCAAGAC	AGAAAAGAAA	AGAAAGGAAG	GGAAAGGGAA	AGGGAAAAGG	AAAAGGAAAA	180
GGAAAAGGAA	AAGGAAAAGA	CAAGACAAAA	CAAGACTTGA	ATTGGATCT	CCTGACTTCA	240
ATTTTATGTT	CTTTCTACAC	CACAATTCC	CTGCTTACTA	AGATGATAAT	TTAGAAACCC	300
CTCGTCCAT	TCTTTACAGC	AAGCTGGAAG	TTTGGTCAAG	TAATTACAAT	AATAGTAACA	360
AATTGAAATA	TTATATGCCA	GGTGTGTTTC	ATTCCCTGCTC	TCACCTAATT	CTCACCACTC	420
TGATATAAAAT	ACAATTGCTG	CCGGGTGTGG	TGGCTCATGC	CTGTAATCCC	GGCACTTTGG	480
GAGACCGAGG	TGGCGGATG	GCAACAA				507

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

TTGGATTGGT	CACTGTGAGG	AAGCCAAATC	GGATCCGAGA	GTCTTTTCT	AAAGGCCAGT	60
ACTGGCCACA	CTTTCTCCTG	CCGCCTTCCT	CAAAGCTGAA	GACACACAGA	GCAAGGGCGCT	120
TCTGTTTAC	TCCCCAATGG	TAACTCCAAA	CCATAGATGG	TTAGCTNCCC	TGCTCATCTT	180
TCCACATCCC	TGCTATTCAG	TATAGTCCGT	GGACCAATCC	AA		222

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

TGTTGCGATC	CATAAAATGCT	GAAATGGAAA	TAAACAACAT	GATGAGGGAG	GATTAAGTTG	60
GGGAGGGAGC	ACATTAAGGT	GGCCATGAAG	TTTGTGGAA	GAAGTGACTT	TTGAACAAAGG	120

CCTTGGTGT	AAGAGCTGAT	GAGAGTGTCC	CAGACAGAGG	GGCCACTGGT	ACAATAGACG	180
AGATGGGAGA	GGGCTGGAA	GGTGTGCGAA	ATAGGAAGGA	GTTCAGCTCG	GTATGAGTCT	240
AGTGAACACA	GAGGGCGAGAG	GCCCTGGTGG	GTGCAGCTGG	AGAGTTATGC	AGAATAACAT	300
TAGGCCCTGT	GGGGGACTGT	AGACTGTCAG	CAATAATCCA	CAGTTGGAT	TTTATTCTAA	360
GAGTGTATGGG	AAGCCGTGGA	AAGGGGGTTA	AGCAAGGAGT	GAAATTATCA	GATTTACAGT	420
GATAAAAATA	AATTGGTCTG	GCTACTGGGG	AAAAAAA	AAA		463

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

TTGGATTGGT	CAACCTGCTC	AACTCTACYT	TTCCCTCCTTC	TTCCTAAAAA	ATTAATGAAT	60
CCAATACATT	AATGCCAAAA	CCCTTGGTT	TTATCAATAT	TTCTGTTAAA	AAGTATTATC	120
CAGAACTGGA	CATAATACTA	CATAATAATA	CATAACAACC	CCTTCATCTG	GATGCAAACA	180
TCTATTAATA	TAGCTTAAGA	TCACTTTCAC	TTTACAGAAG	CAACATCCTG	TTGATGTTAT	240
TTTGATGTTT	GGACCAATCC	AA				262

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GNGGNNNNNN	NNNCAATTCCG	ACTCNGTTCC	CNTGGTANCC	GGTCGACATG	GCCGCGGGAT	60
TACCGCTTGT	NNCTGGGGGT	GTATGGGGA	CTATGACCGC	TTGTAGCTGG	GGGTGTATGG	120
GGGACTATGA	CCGCTTGTAG	MTGGKGGTGT	ATGGGGGACT	ATGACCGCTT	GTCGGGTGGT	180
CGGATAAAACC	GACGCAAGGG	ACGTGATCGA	AGCTGCGTTC	CCGCTCTTTC	GCATCGGTAG	240
GGATCATGGA	CAGCAATATC	CGCATTGCGY	TGAAGGCAGT	CGACCATCGC	GTGCTCGATC	300
AGGCACCGG	CGACATCGCC	GACACCGCAC	GCCGTACCGG	CGCGCTCATC	CGCGGTCCGA	360
TCCCGCTTCC	CACCGCGATC	GAGAAGTTCA	CGGTCAACCG	TGGCCCGCAC	GTCGACAAGA	420
AGTCGCGCGA	GCAGTTCGAG	GTGCGTACCT	ACAAGCGGTC	A		461

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

TGACCGCTTG	TAGCTGGGGG	TGTATGGGGG	ACTACGACCG	CTTGTAGCTG	GGGGTGTATG	60
GGGGACTATG	ACCGCTTGTA	GCTGGGGGTG	TATGGGGGAC	TATGACCGCT	TGTAGCTGGG	120
GGTGTATGGG	GGACTAGGAC	CGCTTGTAGC	TGGGGGTGTA	TGGGGGACTA	TGACCGCTTG	180

TAGCTGGGG TAGCTGGGG ACTACGACCG CTTGTAGCTG GGGGTGTATG GGGGACTATG	240
ACCGCTTGT AACTGGGGTG TATGGGGAC TATGACCGCT TGTGCTGCCT GGGGGATGGG	300
AGGAGAGTTG TGGTTGGGA AAAAAAAA AA	332

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

TACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT	60
GACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT	120
GACCGCTTGT GACCGCTTGT NACNGGGGT GTCTGGGGGA CTATGANNGA NTGTNACTGG	180
GGGTGCTGG GGGNCTATGA NNGANTGTNA CNGGGGGTGT CTGGGGGACT ATGANNGACT	240
GTGCNNCCTG GGGGATCNGA GGAGANTNGN GGNTAGNGAT GGTTNGGGAN A	291

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

TAAGAGGGTA CTGGTTAAAA TACAGGAAAT CTGGGGTAAT GAGGCAGAGA ACCAGGATAC	60
TTTGAGGTCA GGGATGAAAA CTAGAATTTT TTTCTTTTT TTTGCCTGAG AAACCTGCTG	120
CTCTGAAGAG GCCCATGTAT TAATTGCTTT GATCTTCCTT TTCTTACAGC CCTTTCAAGG	180
GCAGAGCCCT CCTTATCCTG AAGGAATCTT ATCCTTAGCT ATAGTATGTA CCCTCTTA	238

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 746 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

TTGGGCACCT TCAATATCAA TAGCTAACAT TTATTGAGTG TTTATCGTAT CATAAAACAC	60
TGTTCTAAGC CTTAAACGT ACTAATTCA TTAATGCTCA TAATCACTTT AGAAGGTGGG	120
TACTAGTATT AGTCTCATTT ACAGATGCAA CATGCAGGCA CAGAGAGTT AATTAACCTG	180
CCCAAGGTAA CACAGCTAAG AAATAGAAAA AATATTGAAT CTGGAAAGTT GGGCTTCTGG	240
GTAACCCACA GAGTCTCAA TGAGCCTGGG GCCTCACTCA GTTTGCTTTT ACAAAGCGAA	300
TGAGTAACAT CACTTAATTC AGTGAGTAGG CCAAATGGAG GTCAGCTACG AGTTTCTGCT	360
GTTCTTGCAAG TGGACTGACA GATGTTACA ACGTCTGGCC ATCAGTWAAT GGACTGATTA	420
TCATTGGGAW GTGGGTGGGC TGAATGTTGG CCAGTGAAGT TTATTCAWGC CATATTTTA	480
TGTTTAGGAT GACTTTGGC TGGCCTAGG GCAAGCTCTG TCTGSCACGG AACACAGAAAT	540
WACACAGGGA CCCCCTCAAT TTCTGGTGTG GCTAGAACCA TGAACCACGT GTTGGGGAA	600

CAAGCGGTCA AAACCTAAGT CGGGCCGGCT GGCAGGGTCC ACCCATATGG GGAAAACCTCC	660
CNACGCGTTT GGAATGCCTN AGCTNGAATT ATTCTAANAG TTGTCCNCNT AAAATTAGCC	720
TGGGCGTTAA TCANGGGTCN NAAGCC	746

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

TGACCGCTTG TCATCTCACCA TGGGGTCCTG CACGCTTTG CCTTTGTAGG AAACCTGACA	60
TTTGTCTGTT TCTTCTTTCT CTTTCCCTC CCATATCCTC CTAATTTCAGG TTTGACTTGT	120
TTGCTGAGGA GGCAGGAGCT AGAGACTGCT GTGAGCTCAT AGGGGTGGGA AGTTTATCCT	180
TCAAGTCCCG CCCACTCCTC ACTGCTTCTC ACCTTCCCT GACCAGGCTT ACAAGTGGGT	240
TCTTGCTCTGC TTTCCCTTG GACCCAAACAA GCCCCGTAA TGAGTGTGCA TGACTCTGAC	300
AGCTGTGGAC TCAGGGTCCT TGGCTACAGC TGCCATGTAA AATATCTCAT CCAGTTCTCG	360
CAAATTGTTA AAATAACCAC ATTTCTTAGA TTCCAGTACC CAAATCATGT CTTTACGAAC	420
TGCTCCTCAC ACCCAGAAGT GGCACAATAA TTCTGGGGA ATTATTACTT TTTTTTTCT	480
CTCTNTNNNC GNNGNNNNNG GNNGNCCAG GAATTACAC NTTGGAAGAC CTGGCCNGAA	540
TTTATTATAN AGGGGAGCCG ATTNTTTTC CTAACACAAA GCGGGTCA	588

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

TTTTTTTTT TTTGGCCTGA GCAACTGAAA TTATGAAATT TCCATATACT CAAAAGAGTA	60
AGACTGAAA AAGATTAAT GTAAAAGTTG TCTTGTATAC AGTAATGTTT AAGATACCTA	120
TTANATTAT AAATGGAAAA TTAGGGCATT TGGATATACA AGTTGAAAAT TCAGGAGTGA	180
GGTTGGGCTG GCTGGGTATA TACTGAAAAC TGTCAGTACA CAGATGACAT CTAAAACCAC	240
AAATCTGGTT TTATTTAGC AGTGTATGT GTCACTCCCA CAAAAGCCTT CCCAATTGGC	300
CTCAGCATAAC ACAACAAGTC ACCTCCCCAC AGCCCTCTAC ACATAAACAA ATTCCCTAGT	360
TTAGTTCAAGG AGGAAATGCG CCCTTTCTC TCCGCTCTAG GTGACCGCAA GGCCCAGTTC	420
TCGTCACCAA GATGTTAAGG GAAGTCTGCC AAAGAGGCAT CTGAAAGGAA ATAAGGGAA	480
TGGGAGTGAC CACAAAGGAA AGCCAAGGAN AAACCTTGGA GACCCTTCT AGANCCCTGG	540
CATTTCACAA CAAAACCTNG GAACAAACCT TGTCTCATCA ATCATTAAAG CCCTTCGTTT	600
GGANNAGACT TTCTGAACTG GGCGCTGAAC ATAANCCTCA TTGAATGTCT TCACAGTCTC	660
CCAGCTGAAG GCACACCTTG GGCCAGAAGG GGAATCTTCC AGGTCCCTCAA NACAGGGCTC	720
GCCCTTTGNC	730

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

TTTTTTTTTT	TTGGCCAGT	ATGATAGTCT	CTACCACAT	ATTGAAGCTC	TTAGGTCA	60
TACACTTAAT	GTGGTTATAG	ATGCTGTTGA	GCTTACTTCT	ACCACCTTGC	TATTTCTCCC	120
GTCTCTTTT	TGTTCCCTTT	CTCTTCTTT	CCTCCCTTAT	TTTATAATTG	AATTTTTAG	180
GATTCTATTT	TATATAGATT	TATCAGCTAT	AACACTTTGT	ATTCTTTGT	TTTGTGGTTC	240
TTCTGTCA	TCAATGTGCA	TCTTAAACTC	ATCACAATCT	ATTTTCAAAT	AATATCATAT	300
AACCTTACAT	ATAATGTAAG	AATCTACCAC	CATATATTC	CATTCTCCC	TTCCATCCTA	360
TGTNTGTCAT	ATTTTTTCCCT	TTATATATGT	TTTAAAGACA	TAATAGTATA	TGGGAGGTTT	420
TTGCTTAAAA	TGTGATCAAT	ATTCCCTCAA	NGAAACGTAA	AAATTCAAAA	TAAATNTCTG	480
TTTATTCTCA	AATNNACCTA	ATATTCCTA	CCATNTCTNA	TACNTTTCAA	GAATCTGAAG	540
GCATTGGTTT	TTTCCGGCTT	AAGAACCTCC	TCTAAAGCAC	TCTAAGCAGA	ATTAAGTCTT	600
CTGGGAGAGG	AATTCTCCCA	AGCTTGGGCC	TTNANNTGTA	CTCCNTNANG	GTTAAANTTT	660
GGCGGGAAA	TAGAAATTCC	AAGTTAACAG	GNTANTTTT	NTTTTTNTTN	TCNCC	715

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

TTTTTTTTTT	TTTCCAACA	CAAAGCACCA	TTATCTTCC	TCACAATT	CAACATAGTT	60
TGATTCCAT	GAAGAGGTTA	TGATTCTAA	AGAAAACATG	GCTACTATAC	TATCAATCAG	120
GGTTAAATCT	TTTTTTTTTG	AGACGGAGTT	TA			152

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

TAAACTCCGT	CCCTTCTTA	ATCAATATGG	AGGCTACCCA	CTCCACATTA	CCTTCTTTTC	60
AAGGGACTGT	TTCCGTAACT	GTTGTGGTA	TTCACGACCA	GGCTTCTAAA	CCTCTTAA	120
CTCCCCAATT	CTGGTGCCAA	CTTGGACAAC	ATGCTTTTT	TTTTTTTTT	TTTTTTTTN	180
GAGACGGAGT	TTA					193

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

TGTTGCGATC CCTTAAGCAT GGGTGTATT	AAAAAAATGG TGGAGAAGAA AATACCTGGA	60
ATTTACGTCT TATCTTTAGA GATTGGGAAG ACCCTGATGG AGGACGTGGA	GAACAGCTTC	120
TTCTTGAATG TCAATTCCA AGTAACAACA GTGTGTCAGG CACTTGCTAA	GGATCCTAAA	180
TTGCAGCAAG GCTACAATGC TATGGGATTC TCCCAGGGAG GCCAATTCT	GAGGGCAGTG	240
GCTCAGAGAT GCCCTTCACC TCCCAGTATC AATCTGATCT CGGTTGGGGG	ACAAACATCAA	300
GGTGTGTTTG GACTCCCTCG ATGCCAGGA GAGAGCTCTC ACATCTGTGA	CTTCATCCGA	360
AAAACACTGA ATGCTGGGGC GTACTCCAAA GTTGTTCAGG AACGCCCTCGT	GCAAGCCGAA	420
TACTGGCATG ACCCATAAAA GGAGGATGTG GATCGCAACA		460

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

TGTTGCGATC CGTTGATAGA ATAGCGACGT GGTAAATGAGT GCATGGCACG	CCTCCGACTT	60
ACCTTCGCCCGTGGGGACCC CGAGTACGTC TACGGCGTCG TCACCTAGAG	TACCCCTCTGG	120
ACGCCCGGGCGCGTTGATT TACCGGAAGC GCGAGCTGCA GTGGGCTTGC	GCCCCCGGCC	180
AAATTCTTTG GGGGGTTTAA GGCCGGGGGG AATTGAGGT ATCTCTATCA	GTATGTAGCC	240
AAGTTGGAAC AGTCGCCATT CCCGAATCG CTTTCTTGA ATCCGCACCG	CCTCCAGCAT	300
TGCCTCATTC ATCAACCTGA AGGCACGCAT AAGTGACGGT TGTGTCTTCA	GCAGCTCCAC	360
TCCATAACTA GCGCGCTCGA CCTCGTCTTC GTACGCGCCA GGTCCGTGCG	TGCGAATTCC	420
CAACTCCGGT GAGTTGCGCA TTTCAAGTTN CGAAACTGTT CGCCTCCACN	ATTTGGCATG	480
TTCACGCATG ACACGGAATA AACTCGTCCA GTACCGGGAA TGGGATCGCA	ACA	533

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

TTTTTTTTTTT TTTCGCCTGAA TTAGCTACAG ATCCTCCTCA CAAGCGGTCA		50
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(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

TGTTGCGATC CAAATAACCC ACCAGCTTCT TGCACACTTC GCAGAAGCCA	CCGTCCTTTG	60
GCTGAGTCAC GTGAACGGTC AGTGCAAGCA GCCGCGTGCC AGAGCAGAGG	TGCAGCATGC	120
TGCACACCCAG CTCAGGGCTG ACCTCCCTCCA GCAGGATGGGA CAGGATGGAG	CTGCCGTACG	180

TGTCCACCAAC	CTCCTGGCAC	TCTTCCGACA	GGGACTTCGG	CAGCTTCGAG	CACATTTGT	240
CAAAGCGTC	GAGTATTCT	TTCTCAGTCT	TGTTGTTGTC	AATCAGCTT	GTCACCTCCT	300
TCACCAAGGAA	TTCACACACC	TCACAGTAAA	CATCAGACTT	TGCTGGGACC	TCGTGCTTCT	360
TAATGGGCTC	CACCAGTCC	AGGGCAGGG	TGACATTCTT	GGAGGCCACT	TTGGCGGGGA	420
CCAGAGTCTG	CATGGGCATC	TCTTCACCT	CATCACAGAA	CCCAACCAGC	GCACAGATCT	480
CCTTGGGTTG	CATGTGCATC	ATCATCTGGG	ATCGCAACA			519

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

TTTTTTTTTT	TTCGGGCGGC	GACCGGACGT	GCACACTCCTCC	AGTAGCGGCT	GCACCGTCGTG	60
CCAATGGCCC	GCTATGAGGA	GGTAGCGGTG	TCCGGCTTCG	AGGAGTTCCA	CCGGGCCGTG	120
GAACAGCACA	ATGGCAAGAC	CATTTTCGCC	TACTTTACGG	GTTCCTAAGGA	CGCCGGGGGG	180
AAAAGCTGGT	GCCCCGACTG	CGTGCAGGCT	GAACCAAGTCG	TACGAGAGGG	GCTGAAGCAC	240
ATTAGTGAAG	GATGTGTGTT	CATCTACTGC	CAAGTAGGAG	AAGAGCCTTA	TTGGAAAGAT	300
CCAAATAATG	ACTTCAGAAA	AAACTTGAAA	GTAACAGCAG	TGCTTACACT	ACTTAAGTAT	360
GGAACACCTC	AAAAACTGGT	AGAATCTGAG	TGTCTTCAGG	CCAACCTGGT	GGAAATGTTG	420
TTCTCTGAAG	ATTAAGATTT	TAGGATGGCA	ATCAAGA			457

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

TTTTTTTTTT	TTGGGCAACA	ACCTGAATAC	CTTTTCAAGG	CTCTGGCTTG	GGCTCAAGCC	60
CGCAGGGGAA	ATGCAACTGG	CCAGGTACCA	GGGCAATCAA	GA		102

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TTTTTTTTTT	TTGGCAATCA	ACAGGTTAA	GTCTTCGGCC	GAAGTTAAC	TCGTGTTTTT	60
GGCAATCAAC	AGGTTAAGT	CTTCGGCCGA	AGTAAATCTC	GTGTTTTG	CAATCAACAG	120
GTTTAAGTCT	TCGGCCGAAG	TTAACCTCGT	GTTTTGGCA	ATCAACAGGT	TTAAGTCTTC	180
GGCCGAAGTT	AATCTCGTG	TTTGGCAAT	CAACAGGTTT	AAGTCTCGG	CCGAAGTTAA	240
TCTCGTGT	TTGGCAATCA	ACAGGTTAA	GTCTTCGGCC	GAAGTTAAC	TCGTGTTTT	300
GGCAATCAAG	AGGTTAAGT	CTTCGGCCGA	AGTTAAC	GTGTTTTG	CAATCAACAG	360

GTTTAAGTCT TCGGCCGAAN TTAATCTCGT GTTTTGGCA ATCAACAGGT TTAANTCTTC
GGCCGAAGTT AATCTCGTGT TTTGGCAAT CAANA

420
455

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

TTTTTTTTTT TTGGCCAATA CCCTTGATGA ACATCAATGT GAAAATCCTC GGTAAAATAC	60
TGGCAAACCA AATCCAGCAG CACATCAAAA AGCTTATCCA CCATGATCAA GTGGGCTTCA	120
TCCCTGGGAT GCAAGGCTGG TTCACACATAA GAAAATCAAT AAATGTAATC CATCACATAA	180
ACAGAACCAA AGACAAAAAC CACATGATTA TCTCAATAGA TGCAGAAAAG GCCTTGGACA	240
AATTCAACAG CCCTTCATGC TAAACACTCT TAATAAACTA GATATTGATG GAATGTATCT	300
CAAATAATA AGAGCTATTG ATGACAAACC CACAGCCAAT ATCATACTGA ATGGGCAAAG	360
ACTGGAAGCA TTCCCTTTGA AAACTGGCAC AAGACAAAGGA TGCCCTCTCT CACCGCTCCT	420
ATTCAACATA GTATTGGAAG TTCTGGCCAG GGCAATCAAG A	461

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 729 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

TTTTTTTTTT TTGGCCAACA CCAAGTCTTC CACGTGGGAG GTTTTATTAT GTTTTACAAC	60
CATGAAAACA TAGGAAGGTG GCTGTTACAG CAAACATTTC AGATAGACGA ATCGGCCAAG	120
CTCCCCAAAC CCCACCTTC CAGCCTCTTC CACACGTCTC CCANAGATTG TTGTCCTTCA	180
CTTGCAAATT CANGGATGTT GGAAGTNGAC ATTTNNAGTN GCNGGAACCC CATCAGTGAA	240
NCANTAAAGCA GAANTACGAT GACTTTGANA NACANCTGAT GAAGAACACN CTACNGANAA	300
CCCTTCTNT CGTGTGTANGA TCTCNNGTCC NTCACTAATG CGGCCCCCTG CNGGTCCACC	360
ATTTGGGAGA ACTCCCCCCN CGTTGGATCC CCCCTTGAGT NTCCCATTTCT NGTCCCCCAN	420
ACCNGNCTTG NGNGNCANTN CNNCCTCNCA CCNTGTTCC CTGNNGTNAA AATNNNGTTT	480
NCCGCCNCCC NAATTCCCAC CCNAATCACA GCGAANCCNG AAGGCCTTCN NAAGTGTGTTA	540
ANGCCCNNG GTTCCCTCNT NTANTTGCAG CCTACCCCTCC CNCTNNNNNT TNCGNGTTGG	600
TCGCGCCCTG GNCNCGCCTN GTTCCCTCTT NNGGNNAACAA CCTNGNTCNN NGGCNCNTCN	660
NNNCTNTCC TNNAACTAGC TNGCCTNTCC NCNCCGNNGN NCANNGCACA TTNCNCNNAC	720
TNTGTNNCC	729

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

TGACCTGACA TGTAGTAGAT ACTTAATAAA TATTTGTGGA ATGAATGGAT GAAAGTGGAGT	60
TACAGAGAAA AATAGAAAAG TACAAATTGT TGTCAAGTGT TTGAAGGAAA ATTATGATCT	120
TTCCCAAAGT TCTGACTTCA TTCTAAGACA GGGTTAGTAT CTCCATACAT AATTTTACTT	180
GCTTTGAAA ATCAAATGAG ATAATCTATT TAGATTGATA ATTATTTAG ACTGGCTATA	240
AACTATTAAG TGCTAGCAAA TATACATTAA AATCTCATTT TCCACCTCTT GTGATATAGC	300
TATGTAGGTG TTGACTTTAA TGGATGTCAG GTCAATCCC	339

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

TGACCTGACA TCCATAACAA AATCTTTCTC CATTATATTC TTCTAGGGGA ATTTCTTGAA	60
AAGCATCCAA AGGAAACAAA TGATGGTAAG ACCGTGCCAA GTGGGGAGCA GACACCAAAG	120
TAAGACCACA GATTTTACAT TCAACAGGTA GCTCACAGTA CTTTGCCCGA CACTGTGGC	180
AGAAAATAGCC TCCATAATGTA AGCCCTGGCT CAGTATTGCC ATCCAAATGC GCCATGCTGA	240
AAGAGGGTTT TGCATCCTGG TCAGATNAAG AAGCAATGGT GTGCTGAGGA AATCCCATA	300
GAATAAGTGA GCATTCAAGAA CTTGAGCTAG CAGGAGGAGG ACTAAGATGA TGTGTGAGCA	360
ACTCTTGTA ATGGCTTTCA TCTAAAATAA CATGGTACGT GCCACCAAGT TCACGAGCAA	420
GTACAGTGCA AACCGGAAC TCTGCAGACA ATCCAATAAC AGATACTCTA ATTTTAGCTG	480
CCTTTAGGGT CTTGATTAAA TCATAAAATAT TAGATGGATC GCAAGTTGTA AGGNTGCTAA	540
AAGATGATTA GTACTTCTCG ACTTGTATGT CCAGGCATGT TGTTTAAAN TCTGCCTTAG	600
NCCCTGCTTA GGGAAATTAA TAAAGAAGAT GGCTCTCCAT GTTCANGGTC AATCACNAAT	660
TGCC	664

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

TGACCTGACA TTGAGGAAGA GCACACACCT CTGAAATTCC TTAGGTTCAAG AAGGGCATT	60
GACACAGAGT GGGCCTCTGA TAATTCTATGA AATGCATTCT GAAGTCATCC AGAATGGAGG	120
CTGCAATCTG CTGTGCTTGC GGGGTGCT CACTGTGCTC CTGGATATCA CACAAAAGCT	180
GCAATCCTTC TTCTTCAACT AACATTTGC AGTATTGCT GGGATTTTA CTGCAGACAT	240
GATACATAGC CCATAGTGCC CAGAGCTGAA CCTCTGGTTG AGAGAAAGTTG CCAAGGAGCG	300
GGAAAAATGT CTTGAAAGAT CTATAGGTCA CCAATGCTGT CATCTTACAA CTTGAACCTG	360
GCCAATTCTG TATGGTTGCA TGCAGATCTT GGAGAAGAGT ACGCCTCTGG AAGTCACGGG	420
ATATCCAAAN CTGTCTGTCA GATGTCAGGT CA	452

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

TTTTTTTTTT	TTCGGCAAGG	CAAATTTACT	TCTGCAAAAG	GGTGCCTGCTT	GCACCTTTGG	60
CCACTGCGAG	AGCACACCAA	ACAAAGTAGG	GAAGGGGTTT	TTATCCCTAA	CGCGGTTATT	120
CCCTGGTTCT	GTGCGTGTC	CCCATGGCT	GGAGTCAGAC	TGCACAACTCT	ACACTGACCC	180
AACTGGCTAC	TGTTTAAAAT	TGAATATGAA	TAATTAGGTA	GGAAGGGGA	GGCTGTTGT	240
TACGGTACAA	GACGTGTTG	GGCATGTCAG	GTCA			274

(2) INFORMATION FOR SEQ ID NO:280:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

TACCTGACAT	GGAGAAATAA	CTTGTAGTAT	TTTGCCTGCA	ATGGAATACT	ATATGAGGGT	60
GAAAATGAAT	GAACTAGCAA	TGCGTGTATC	AACATGAATA	AATCCCCAAA	ACATAATAAT	120
GTTGAATGGA	AAAGGTGAGT	TTCAGAAGGA	TATATATGCC	CTCTAAATCC	ATTTATGTAA	180
ACCTTTAAAA	AACTACATTA	TTTATGGTCA	TAAGTCCATC	CAGAAAATAT	TTAAAAACCT	240
ACATGGGATT	GATAACTACT	GATGTCAGGT	CA			272

(2) INFORMATION FOR SEQ ID NO:281:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

TTTTTTTTTT	TTGGCCAATA	GCATGATTAA	AACATTGGAA	AAAGTCAAAT	GAGCAATGCG	60
AATTTTTATG	TTCTCTTGAA	TAATCAAAAG	AGTAGGCAC	ATTGGTTCT	CATTCTTGAA	120
TAGCATTAAAT	CAGAAAATAT	TGCATAGCCT	CTAGCCTCCT	TAGAGTAGGT	GTGCTCTTC	180
AAATATATCA	TAGTCCCACA	GTTTATTTC	TGTATATTTT	CTGCCTGAAT	CACATAGACA	240
TTTGAATTG	CAACGCCTGA	TGTAAATATA	AAAATTCTTA	CCAATCAGAA	ACATAGCAAG	300
AAATTCAGGG	ACTTGGTCAT	YATCAGGGTA	TGACAGCANA	TCCCTGTARA	AACACTGATA	360
CACACTCACA	CACGTATGCA	ACGTGGAGAT	GTGCGYTTWW	KKKTWYWCWM	RMRYCRWCN	420
AATCACTTAN	N					431

(2) INFORMATION FOR SEQ ID NO:282:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

ATTCGATTG ATGCTTGAGC CCAGGAGTTC AAGACTGCAG TGAGCCACTG CACTTCAGGC	60
TGGACAAACAG AGCGAGTCCC TGTGCAAAAA AAAAAAAA	98

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

TTTTTTTTT TTCGCAAGCA CGTGCAC TTT ATTGAATGAC ACTGTAGACA GGTGTGTGGG	60
TATAAACTGC TGTATCTAGG GGCAGGACCA AGGGGGCAGG GGCAACAGCC CCAGCGTGCA	120
GGGCCASCAT TGCACAGTGG ASTGCAAAGG TTGCAGGCTA TGGCGGGCTA CTAVTAACCC	180
CGTTTTCT GTATTATCTG TAACATAATA TGGTAGACTG TCACAGAGCC GAATWCCART	240
HACASGATGA ATCCA AWG GT CAYGAGGATG CCCASAATCA GGGCC CASAT STTCAGGCAC	300
TTGGCGGTGG GGGCATASGC CTGKGCCCCG GTCACGTCS CAA CWTCTY CCTGTCCCTA	360
CMCTTGA WTC CNCNCCTTNN NNTNCNTNA TNTGCCCGCC CNCCTCCTNG NGTCAACCNG	420
NATCTGCACT ANCTCCCTCN CCCCTTNTGG ANTCTCNTCC TTCAANTAAN NTTATCCTTN	480
ACNCCCCCCT CNCCTTCCC CTNCCNCCCN TNATCCNGN NCCNCTATCA NTCNTNCCT	540
CNCTNTNCTN CNNATCGTTC CNCCTNN TAA CTACNCTTN NACNANNCT CACTNATNCC	600
NGNNANTTCT TTCCCTCCCT CCCNACGCNN TGC GTGC GCC CGTCTNGCCT NNNCTNCGNA	660
CCCNNACTTT ATTACCTTT NCACCC TAGC NCTCTACTTN ACCCANCNC TCCTACCTCC	720
NGGNCCACCC NNCCCTNATC NCTNNCTCTN TCNNCTCNTT CCCC	764

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

CAAGTGTAGG CACAGTGATG AAAGCCTGGA GCAAACACAA TCTGTGGGTA ATTAACGTTT	60
ATTTCTCCCC TTCCAGGAAC GTCTTGATG GATGATCAA GATCAGCTCC TGGTCAACAT	120
AAATAAGCTA GTTTAAGATA CGTTCCCTA CACTTGA	157

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

ATTCGATTGT ACTCAGACAA CAATATGCTA AGTGGAAAGAA GTCAGTCACA AAAGACCACA	60
TACTGTATGA CTTCATTTAC ATTAAGTGTCA CAGAATAGGC AAATCCGTAG AGACAGAAAG	120
TAGATGAGCA GCTGCCTAGG TCTGAGTACA	150

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

ATTCGATTTC	TTTTTTTTTG	GCCATGATGA	AATTCTTACT	CCCTCAGATT	TTTTGTCTGG	60
ATAAATGCAA	GTCTCACAC	CAGATGTGAA	ATTACAGTAA	ACTTTGAAGG	AATCTCCTGA	120
GCAACCTTGG	TTAGGATCAA	TCCAATATTTC	ACCATCTGGG	AAGTCAGGAT	GGCTGAGTTG	180
CAGGTCTTTA	CAAGTTCGGG	CTGGATTGGT	CTGAGTACA			219

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

ATTCGATTCT	TGAGGCTTAC	AGGAGCTAGG	AGAAGAGGCA	TGGAACAAAT	TTTCCCTCAT	60
ATCCATACTC	AGAAGGAACC	AACCCTGCTG	ACACCTTAAT	TCAGCTTCT	GGCCTCTAGA	120
ACTGTGAGAG	AGTACATTTC	TCTTGTTTA	AGCCAAGAGA	ATCTGTCTTT	TGGTACTTTA	180
TATCATAGCC	TCAAGA					196

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

ATTCGATTTC	AGTCCAGTCC	CAGAACCCAC	ATTGTCAATT	ACTACTCTGT	ARAAGATTCA	60
TTTGTGAAA	TTCATTGAGT	AAAACATTAA	TGATCCCTTA	ATATATGCCA	ATTACCATGC	120
TAGGTACTGA	AGATTCAAGT	GACCGAGATG	CTAGCCCTTG	GGTTCAAGTG	ATCCCTCTCC	180
CAGAGTGCAC	TGGACTGAA					199

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

ATTCGATTCT TGAGGCTACA AACCTGTACA GTATGTTACT CTACTGAATA CTGTAGGCAA	60
TAGTAATACA GAAGCAAGTA TCTGTATATG TAAACATTAA AAAGGTACAG TGAAACTTCA	120
GTATTATAAT CTTAGGGACC ACCATTATAT ATGTGGTCCA TCATTGGCCA AAAAAAAA	180
AA	182

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

GGCACGAGGA GAAATGTAAT TCCATATTTT ATTTGAAACT TATTCCATAT TTTAATTGGA	60
TATTGAGTGA TTGGGTTATC AAACACCCAC AAACCTTAAT TTTGTTAAAT TTATATGGCT	120
TTGAAATAGA AGTATAAGTT GCTACCATTT TTTGATAACA TTGAAAGATA GTATTTTAC	180
ATCTTTAATC ATCTTGGAAA ATACAAGTCC TGTGAACAAC CACTCTTCAC CCTAGCAGCA	240
TGAGGCCAAA AGTAAAGGCT TTAAATTATA ACATATGGGA TTCTTAGTAG TATGTTTTT	300
TCTTGAAACT CAGTGGCTCT ATCTAACCTT ACTATCTCCT CACTCTTCCT CTAAGACTAA	360
ACTCTAGGCT CTTAAAATC TGCCCACACC AATCTTAGAA GCTCTGAAAA GAATTTGTCT	420
TTAAATATCT TTTAATAGTA ACATGTATTT TATGGACCAA ATTGACATTT TCGACTATTT	480
TTTCCAAAAA AGTCAGGTGA ATTCAGCAC ACTGAGTTGG GAATTCTTA TCCCAGAAGA	540
CCAACCAATT TCATATTAT TTAAGATTGA TTCCATACCTC CGTTTCAAG GAGAATCCCT	600
GCAGTCTCCT TAAAGGTAGA ACAAAACTT TCTATTTTT TTTCACCATT GTGGGATTGG	660
ACTTTAAGAG GTGACTCTAA AAAAACAGAG AACAAATATG TCTCAGTTGT ATTAAGCACG	720
GACCCATATT ATCATATTCA CTTAAAAAA TGATTCCTG TGACCTTTT GGCAACTTCT	780
CTTTTCAATG TAGGGAAAAA CTTAGTCACC CTGAAAACCC ACAAAATAAA TAAAACTTGT	840
AGATGTGGGC AGAAGGTTTC GGGGTGGACA TTGTATGTGT TAAATTAAA CCCTGTATCA	900
CTGAGAACGCT GTTGTATGGG TCAGAGAAAA TGAATGCTTA GAAGCTGTT ACATCTCAA	960
GAGCAGAACG AAACACACATG TCTCAGCTAT ATTATTATTT ATTGTTTATG CATAAAGTG	1020
ATCATTCTT CTGTATTAAT TTCAAAGGG TTTTACCCCTC TATTAAATG CTTTGAAAAA	1080
CAGTGCATTG ACAATGGTT GATATTTC TTTAAAGAA AAATATAATT ATGAAAGCCA	1140
AGATAATCTG AAGCCTGTT TATTAAATTTT CTTTTATGT TCTGTGGTT ATGTTGTTG	1200
TTTGTGTT TCTATTTGT TGTTTTTTA CTTTGTGTT TGTTTGTT TGTTTGTT	1260
KGCATACTAC ATGCAGTTCT TTAACCAATG TCTGTTGGC TAATGTAATT AAAGTTGTTA	1320
ATTTATATGA GTGCATTCA ACTATGTCAA TGGTTCTTA ATATTATG TGTAGAAGTA	1380
CTGGTAATTT TTTTATTTAC AATATGTTA AAGAGATAAC AGTTTGATAT GTTTTCATGT	1440
GTTTATAGCA GAAGTTATTT ATTTCTATGG CATTCCAGCG GATATTGTTG TGTTTGCGAG	1500
GCATGCAGTC AATATTTGT ACAGTTAGTG GACAGTATTG AGCAACGCCT GATAGCTTCT	1560
TTGGCCTTAT GTAAATAAA AAGACCTGTT TGGGATGTAT TTTTATTTT TAAAAAAA	1620
AAAAAAA AAAA AAAAAA AAAAAA	1646

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

TCATCACCAT	TGCCAGCAGC	GGCACCGTTA	GTCAGGTTT	CTGGGAATCC	CACATGAGTA	60
CTTCCGTGTT	CTTCATTCTT	CTTCAATAGC	CATAAATCTT	CTAGCTCTGG	CTGGCTGTTT	120
TCACCTCCTT	TAAGCCTTG	TGACTCTTCC	TCTGATGTCA	GCTTTAAGTC	TTGTTCTGGA	180
TTGCTGTTT	CAGAAGAGAT	TTTTAACATC	TGTTTTCTT	TGTAGTCAGA	AAGTAACTGG	240
CAAATTACAT	GATGATGACT	AGAAACAGCA	TACTCTCTGG	CCGTCTTCC	AGATCTTGAG	300
AAGATAACATC	AACATTTGC	TCAAGTAGAG	GGCTGACTAT	ACTTGCTGAT	CCACAACATA	360
CAGCAAGTAT	GAGAGCAGTT	CTTCCATATC	TATCCAGCGC	ATTAAATTC	GCTTTTTCT	420
TGATTAACAAA	TTTCACCACT	TGCTGTTTT	GCTCATGTAT	ACCAAGTAGC	AGTGGTGTGA	480
GGCCATGCTT	GTTTTTGAT	TCGATATCAG	CACCGTATAA	GAGCAGTGCT	TTGGCCATTA	540
ATTTATCTTC	ATTGTAGACA	GCATAGTGT	GAGTGGTATT	TCCATACTCA	TCTGGAATAT	600
TTGGATCAGT	GCCATGTTCC	AGCAACATTA	ACGCACATTC	ATCTCCTGG	CATTGTACGG	660
CCTTTGTCAG	AGCTGTCTC	TTTTGTTGT	CAAGGACATT	AAGTGACAT	CGTCTGTCCA	720
GCACGAGTTT	TACTACTTCT	GAATTCCCAT	TGGCAGAGGC	CAGATGTAGA	GCAGTCCTCT	780
TTTGCTTGTG	CCTCTTGTTC	ACATCCGTGT	CCCTGAGCAT	GACGATGAGA	TCCTTCTGG	840
GGACTTTACC	CCACCAAGGCA	GCTCTGTGGA	GCTTGTCCAG	ATCTTCTCCA	TGGACGTGGT	900
ACCTGGGATC	CATGAAGGCG	CTGTCATCGT	AGTCTCCCCA	AGCGACCACG	TTGCTCTTGC	960
CGCTCCCTG	CAGCAGGGGA	AGCAGTGGCA	GCACCACTTG	CACCTCTTGC	TCCCAGCGT	1020
CTTCACAGAG	GAGTCGTTGT	GGTCTCCAGA	AGTCCCCACG	TTGCTCTTGC	CGCTCCCCCT	1080
GTCCATCCAG	GGAGGAAGAA	ATGCAGGAAA	TGAAAGATGC	ATGCACGATG	GTATACTCCT	1140
CAGCCATCAA	ACTTCTGGAC	AGCAGGTCAC	TTCCAGCAAG	GTGGAGAAAG	CTGTCCACCC	1200
ACAGAGGATG	AGATCCAGAA	ACCACAATAT	CCATTACAAA	ACAAACACTT	TTCAGCCAGA	1260
CACAGGTA	GAAATCATGT	CATCTCGGGC	AACATGGTGG	AACCTACCCA	ATCACACATC	1320
AAGAGATGAA	GACACTGCAG	TATATCTGCA	CAACGTAATA	CTCTTCATCC	ATAACAAAAT	1380
AATATAATT	TCCTCTGGAG	CCATATGGAT	GAACTATGAA	GGAAGAACTC	CCCGAAGAAG	1440
CCAGTCGCAG	AGAAGCCACA	CTGAAGCTCT	GTCCTCAGCC	ATCAGCGCA	CGGACAGGAR	1500
TGTGTTTCTT	CCCCAGTGT	GCAGCCTCAA	GTTATCCCGA	AGCTGCCGCA	GCACACGGTG	1560
GCTCCTGAGA	AACACCCCAG	CTCTTCCGGT	CTAACACAGG	CAAGTCAATA	AATGTGATAAA	1620
TCACATAAAC	AGAATTAAAAA	GCAAAGTCAC	ATAAGCATCT	CAACAGACAC	AGAAAAGGCA	1680
TTTGACAAAAA	TCCAGCATCC	TTGTATTAT	TGTTGCAGTT	CTCAGAGGAA	ATGTTCTAA	1740
CTTTTCCCA	TTTAGTATTA	TGTTGGCTGT	GGGCTTGTCA	TAGTGGTTT	TTATTACTTT	1800
AAGGTATGTC	CCTTCTATGC	CTGTTTGCT	GAGGGTTTA	ATTCTCGTGC	C	1851

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

TCATCACCAT	TGCCAGCAGC	GGCACCGTTA	GTCAGGTTT	CTGGGAATCC	CACATGAGTA	60
CTTCCGTGTT	CTTCATTCTT	CTTCAATAGC	CATAAATCTT	CTAGCTCTGG	CTGGCTGTTT	120
TCACCTCCTT	TAAGCCTTG	TGACTCTTCC	TCTGATGTCA	GCTTTAAGTC	TTGTTCTGGA	180
TTGCTGTTT	CAGAAGAGAT	TTTTAACATC	TGTTTTCTT	TGTAGTCAGA	AAGTAACTGG	240
CAAATTACAT	GATGATGACT	AGAAACAGCA	TACTCTCTGG	CCGTCTTCC	AGATCTTGAG	300
AAGATAACATC	AACATTTGC	TCAAGTAGAG	GGCTGACTAT	ACTTGCTGAT	CCACAACATA	360
CAGCAAGTAT	GAGAGCAGTT	CTTCCATATC	TATCCAGCGC	ATTAAATTC	GCTTTTTCT	420
TGATTAACAAA	TTTCACCACT	TGCTGTTTT	GCTCATGTAT	ACCAAGTAGC	AGTGGTGTGA	480
GGCCATGCTT	GTTTTTGAT	TCGATATCAG	CACCGTATAA	GAGCAGTGCT	TTGGCCATTA	540
ATTTATCTTC	ATTGTAGACA	GCATAGTGT	GAGTGGTATT	TCCATACTCA	TCTGGAATAT	600
TTGGATCAGT	GCCATGTTCC	AGCAACATTA	ACGCACATTC	ATCTCCTGG	CATTGTACGG	660
CCTTGTCTG	AGCTGTCTC	TTTTGTTGT	CAAGGACATT	AAGTGACAT	CGTCTGTCCA	720
GCACGAGTTT	TACTACTTCT	GAATTCCCAT	TGGCAGAGGC	CAGATGTAGA	GCAGTCCTCT	780

TTTGCTTGTGTC CCTCTTGTTC ACATCCGTGT CCCTGAGCAT GACGATGAGA TCCTTTCTGG	840
GGACTTTTACCC ACCCAGGCA GCTCTGTGGA GCTTGTCCAG ATCTTCTCCA TGGACGTGGT	900
ACCTGGGATC CATGAAGGCG CTGTCATCGT AGTCTCCCCA AGCGACCACG TTGCTCTTGC	960
CGCTCCCCCTG CAGCAGGGGA AGCAGTGGCA GCACCACTTG CACCTCTTGC TCCCAAGCGT	1020
CTTCACAGAG GAGTCGTTGT GGTCTCCAGA AGTGCCACG TTGCTCTTGC CGCTCCCCCT	1080
GTCCATCCAG GGAGGAAGAA ATGCAGGAAA TGAAAGATGC ATGCACGATG GTATACTCCT	1140
CAGCCATCAA ACTTCTGGAC AGCAGGTCAC TTCCAGCAAG GTGGAGAAAG CTGTCACCC	1200
ACAGAGGATG AGATCCAGAA ACCACAATAT CCATTACAA ACAAACACTT TTCAGCCAGA	1260
CACAGGTACT GAAATCATGT CATCTGCGGC AACATGGGG AACCTACCC AATCACACATC	1320
AAGAGATGAA GACACTGCAG TATATCTGCA CAACGTAATA CTCTTCATCC ATAACAAAAT	1380
AATATAATTT TCCTCTGGAG CCATATGGAT GAACTATGAA GGAAGAACTC CCCGAAGAAG	1440
CCAGTCGCAG AGAAGCCACA CTGAAGCTCT GTCCTCAGCC ATCAGCGCCA CGGACAGGAR	1500
TGTGTTCTT CCCCAGTGAT GCAGCCTCAA GTTATCCCGA AGCTGCCGCA GCACACGGTG	1560
GCTCCTGAGA AACACCCAG CTCTTCCGGT CTAACACAGG CAAGTCAATA AATGTGATAA	1620
TCACATAAAC AGAATTAAAA GCAAAGTCAC ATAAGCATCT CAACAGACAC AGAAAAGGCA	1680
TTTGACAAAAA TCCAGCATCC TTGTATTAT TGTTGCAGTT CTCAGAGGAA ATGCTTCTAA	1740
CTTTTCCCCA TTTAGTATTA TGTTGGCTGT GGGCTTGTCA TAGTTGGTT TTATTACTTT	1800
AAGGTATGTC CCTCTATGC CTGTTTGCT GAGGGTTTTA ATTCTCGTGC C	1851

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

CTTGAGCTTC CAAATAYGGA AGACTGGCCC TTACACASGT CAATGTTAAA ATGAATGCAT	60
TTCAGTATTG TGAAGATAAA ATTRGTAGAT CTATACCTTG TTTTTGATT CGATATCAGC	120
ACCRTATAAG AGCAGTGCTT TGGCCATTAA TTTATCTTC ATTRTAGACA GCRTAGTGYA	180
GAGTGGTATT TCCATACTCA TCTGGAATAT TTGGATCAGT GCCATGTTCC AGCAACATTA	240
ACGCACATTC ATCTTCCTGG CATTGTACGG CCTGTCAGTA TTAGACCCAA AAACAAATTA	300
CATATCTTAG GAATTCAAAA TAACATTCCA CAGCTTCAC CAACTAGTTA TATTTAAAGG	360
AGAAAACCTA TTTTATGCC ATGTATTGAA ATCAAACCCA CCTCATGCTG ATATAGTGG	420
CTACTGCATA CCTTTATCAG AGCTGTCCTC TTTTGTTGT CAAGGACATT AAGTTGACAT	480
CGTCTGTCCA GCAGGAGTTT TACTACTCT GAATTCCCAT TGGCAGAGGC CAGATGTAGA	540
GCAGTCCTAT GAGAGTGGAGA AGACTTTTA GGAAATTGTA GTGCACTAGC TACAGCCATA	600
GCAATGATTC ATGTAACCTGC AAACACTGAA TAGCCTGCTA TTACTCTGCC TTCAAAAAAA	660
AAAAAAAAAA	668

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GGGTGCCCA GGGGGSGCGT GGGCTTCCT CGGGTGGGTG TGGGTTTCC CTGGGTGGGG	60
TGGGCTGGGC TRGAATCCCC TGCTGGGTT GGCAGGTTT GGCTGGGATT GACTTTTYTC	120
TTCAACAGA TTGGAAACCC GGAGTTACCT GCTAGTTGGT GAAACTGGTT GGTAGACGCG	180

ATCTGTTGGC TACTACTGGC TTCTCCTGGC TGTAAAAGC AGATGGTGGT TGAGGTTGAT	240
TCCATGCCGG CTGCTTCTTC TGTGAAGAAG CCATTGGTC TCAGGAGCAA GATGGGCAAG	300
TGGTGTGCC GTTGCTTCCC CTGCTGCAGG GAGAGCGGCA AGAGCAACGT GGGCACTTCT	360
GGAGACCACG ACGACTCTGC TATGAAGACA CTCAGGAGCA AGATGGGCAA GTGGTGCCGC	420
CACTGCTTCC CCTGCTGCAG GGGGAGTGGC AAGAGCAACG TGGCGCTTC TGGAGACCAC	480
GACGAYTCTG CTATGAAGAC ACTCAGGAAC AAGATGGGCA AGTGGTGCTG CCACTGCTTC	540
CCCTGCTGCA GGGGGAGCRG CAAGAGCAAG GTGGCGCTT GGGGAGACTA CGATGACAGT	600
GCCTTCATGG AGCCCAGGTA CCACGTCCGT GGAGAAGATC TGGACAAGCT CCACAGAGCT	660
GCCTGGTGGG GTAAAGTCCC CAGAAAGGAT CTCATCGTCA TGCTCAGGTA CACTGACGTG	720
AACAAGAAGG ACAAGCAAA GAGGACTGCT CTACATCTGG CCTCTGCCAA TGGGAATTCA	780
GAAGTAGTAA AACTCSTGCT GGACAGACGA TGTCAACTTA ATGTCCTTGA CAACAAAAAG	840
AGGACAGCTC TGAYAAAGGC CGTACAATGC CAGGAAGATG AATGTGCGTT AATGTTGCTG	900
GAACATGGCA CTGATCCAAA TATTCCAGAT GAGTATGGAA ATACCACTCT RACTAYGCT	960
RTCTAYAATG AAGATAAATT AATGGCCAAA GCACTGCTCT TATAYGGTGC TGATATCGAA	1020
TCAAAAAACA AGGTATAGAT CTACTAATTT TATCTTCAAAT AACTGAAAT GCATTCAATT	1080
TAACATTGAC GTGTGTAAGG GCCAGCTTC CGTATTGGA AGCTCAAGCA TAACTTGAAT	1140
GAAAATATTT TGAAATGACC TAATTATCTM AGACTTTATT TTAAATATTG TTATTTCAA	1200
AGAAGCATTG GAGGGTACAG TTTTTTTTT TTAAATGCAC TTCTGGTAA TACTTTGTT	1260
GAAAACACTG AATTGTAAA AGGTAATACT TACTATTGTT CAATTTTCC CTCCTAGGAT	1320
TTTTTCCCG TAATGAATGT AAGATGGCAA AATTTGCCCT GAAATAGGTT TTACATGAAA	1380
ACTCCAAGAA AAGTTAAACA TGTTTCAGTG AATAGAGATC CTGCTCCTT GGCAAGTTCC	1440
TAAAAAACAG TAATAGATAC GAGGTGATGC GCCTGTCAGT GGCAAGGTTT AAGATATTTC	1500
TGATCTCGTG CC	1512

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1853 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GGGTGCCCCA GGGGGSGCGT GGGCTTCCT CGGGTGGGTG TGGGTTTCC CTGGGTGGGG	60
TGGGCTGGGC TRGAATCCCC TGCTGGGTT GGCAGGTTT GGCTGGGATT GACTTTTYTC	120
TTCAAACAGA TTGGAAACCC GGAGTTACCT GCTAGTTGGT GAAACTGGTT GGTAGACGCG	180
ATCTGTTGGC TACTACTGGC TTCTCCTGGC TGTAAAAGC AGATGGTGGT TGAGGTTGAT	240
TCCATGCCGG CTGCTTCTTC TGTGAAGAAG CCATTGGTC TCAGGAGCAA GATGGGCAAG	300
TGGTGTGCC GTTGCTTCCC CTGCTGCAGG GAGAGCGGCA AGAGCAACGT GGGCACTTCT	360
GGAGACCACG ACGACTCTGC TATGAAGACA CTCAGGAGCA AGATGGGCAA GTGGTGCCGC	420
CACTGCTTCC CCTGCTGCAG GGGGAGTGGC AAGAGCAACG TGGCGCTTC TGGAGACCAC	480
GACGAYTCTG CTATGAAGAC ACTCAGGAAC AAGATGGGCA AGTGGTGCTG CCACTGCTTC	540
CCCTGCTGCA GGGGGAGCRG CAAGAGCAAG GTGGCGCTT GGGGAGACTA CGATGACAGY	600
GCCTTCATGG AKCCCAGGTA CCACGTCCRT GGAGAAGATC TGGACAAGCT CCACAGAGCT	660
GCCTGGTGGG GTAAAGTCCC CAGAAAGGAT CTCATCGTCA TGCTCAGGGA CACKGAYGTG	720
AACAAGARGG ACAAGCAAA GAGGACTGCT CTACATCTGG CCTCTGCCAA TGGGAATTCA	780
GAAGTAGTAA AACTCSTGCT GGACAGACGA TGTCAACTTA ATGTCCTTGA CAACAAAAAG	840
AGGACAGCTC TGAYAAAGGC CGTACAATGC CAGGAAGATG AATGTGCGTT AATGTTGCTG	900
GAACATGGCA CTGATCCAAA TATTCCAGAT GAGTATGGAA ATACCACTCT RACTAYGCT	960
RTCTAYAATG AAGATAAATT AATGGCCAAA GCACTGCTCT TATAYGGTGC TGATATCGAA	1020
TCAAAAAACA AGCATGGCCT CACACCACTG YTACTTGGTR TACATGAGCA AAAACAGCAA	1080
GTSGTGAAT TTTAATYAA GAAAAAAAGCG AATTAAAT GCRCTGGATA GATATGGAAG	1140
RACTGCTCTC ATACTTGCTG TATGTTGTGG ATCAGCAAGT ATAGTCAGCC YTCTACTTGA	1200
GCAAAATRTT GATGTATCTT CTCAAGATCT GGAAAGACGG CCAGAGAGTA TGCTGTTCT	1260

AGTCATCATC ATGTAATTTG CCAGTTACTT TCTGACTACA AAGAAAAACA GATGTTAAAA	1320
ATCTCTTCTG AAAACAGCAA TCCAGAACAA GACTTAAAGC TGACATCAGA GGAAGAGTCA	1380
CAAAGGCTTA AAGGAAGTGA AAACAGCCAG CCAGAGGCAT GGAAACTTTT AAATTTAAC	1440
TTTTGGTTA ATGTTTTTTT TTTTGCCTT AATAATATTA GATAGTCCC AATGAAATWA	1500
CCTATGAGAC TAGGCTTGA GAATCAATAG ATTCTTTTT TAAGAATCTT TTGGCTAGGA	1560
CGGGTGTCTC ACGCCTGTAA TTCCAGCACC TTGAGAGGCT GAGGTGGGCA GATCACGAGA	1620
TCAGGAGATC GAGACCACAC TGGCTAACAC GGTGAAACCC CATCTCTACT AAAAATACAA	1680
AAACTTAGCT GGGTGTGGTG GCGGGTGCCT GTAGTCCCAG CTACTCAGGA RGCTGAGGCA	1740
GGAGAATGGC ATGAACCCGG GAGGTGGAGG TTGCAGTGAG CCGAGATCCG CCACTACACT	1800
CCAGCCTGGG TGACAGAGCA AGACTCTGTC TCAAAAAAAA AAAAAAAA AAA	1853

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

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TTTCCTCTGA GAACTGCAAC AATAAATACA AGGATGCTGG ATTGTTGTCAA ATGCCCTTTC	180
TGTGTCTGTT GAGATGCTTA TGTGACTTTG CTTTTAATTC TGTTTATGTG ATTATCACAT	240
TTATTGACTT GCCTGTGTTA GACCGGAAGA GCTGGGGTGT TTCTCAGGAG CCACCGTGTG	300
CTGCGGCAGC TTCGGGATAA CTTGAGGCTG CATCACTGGG GAAGAAACAC AYTCCTGTCC	360
GTGGCGCTGA TGGCTGAGGA CAGAGCTTCA GTGTGGCTTC TCTGCGACTG GCTTCTTCGG	420
GGAGTTCTTC CTTCATAGTT CATCCATATG GCTCCAGAGG AAAATTATAT TATTTTGTAA	480
TGGATGAAGA GTATTACGTT GTGCAGATAT ACTGCAGTGT CTTCATCTCT TGATGTGTGA	540
TTGGGTAGGT TCCACCATGT TGCCGCAGAT GACATGATT CAGTACCTGT GTCTGGCTGA	600
AAAGTGTGTTG TTTGTGAATG GATATTGTGG TTTCTGGATC TCATCCTCTG TGGGTGGACA	660
GCTTTCTCCA CTTGCTGGA AGTGACCTGC TGTCCAGAAG TTTGATGGCT GAGGAGTATA	720
CCATCGTGCA TGCATCTTTC ATTTCTGCA TTTCTTCCTC CCTGGATGGA CAGGGGGAGC	780
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AGCAAGAGGT GCAAGTGGTG CTGCCACTGC TTCCCCTGCT GCAGGGGAGC GGCAAGAGCA	900
ACGTGGTCGC TTGGGGAGAC TACGATGACA GCGCCTTCAT GGATCCCAGG TACACGTCC	960
ATGGAGAAGA TCTGGACAAG CTCCACAGAG CTGCCTGGTG GGGTAAAGTC CCCAGAAAGG	1020
ATCTCATCGT CATGCTCAGG GACACGGATG TGAACAAGAG GGACAAGCAA AAGAGGACTG	1080
CTCTACATCT GGCTCTGCC AATGGGAATT CAGAAGTAGT AAAACTCGTG CTGGACAGAC	1140
GATGTCACT TAATGTCCTT GACAACAAAA AGAGGACAGC TCTGACAAAG GCCGTACAAT	1200
GCCAGGAAGA TGAATGTGCG TTAATGTTGC TGGAACATGG CACTGATCCA AATATTCCAG	1260
ATGAGTATGG AAATACCACT CTACACTATG CTGTCTACAA TGAAGATAAA TTAATGGCCA	1320
AAGCACTGCT CTTATACGGT GCTGATATCG AATCAAAAAA CAAGCATGGC CTCACACAC	1380
TGCTACTTGG TATACATGAG CAAAAACAGC AAGTGGTGAA ATTTTTAAC TAAAGAAAAAG	1440
CGAATTAAA TGCGCTGGAT AGATATGGAA GAACTGCTCT CATACTTGCT GTATGTTGTG	1500
GATCAGCAAG TATAGTCAGC CCTCTACTTG AGCAAAATGT TGATGTATCT TCTCAAGATC	1560
TGGAAAGACG GCCAGAGAGT ATGCTGTTTC TAGTCATCAT CATGTAATTT GCCAGTTACT	1620
TTCTGACTAC AAAGAAAAAC AGATGTTAAA AATCTCTTCT GAAAACAGCA ATCCAGAAC	1680
AGACTTAAAG CTGACATCAG AGGAAGAGTC ACAAAAGGCTT AAAGGAAGTG AAAACAGCCA	1740
GCCAGAGGCA TGGAAACTTT TAAATTAAA CTTTTGGTTT AATGTTTTTT TTTTTGCT	1800
TAATAATATT AGATAGTCCC AAATGAAATW ACCTATGAGA CTAGGCTTTG AGAATCAATA	1860
GATTCTTTTT TTAAGAATCT TTTGGCTAGG AGCGGTGTCT CACGGCTGTA ATTCCAGCAC	1920
CTTGAGAGGC TGAGGTGGGC AGATCACGAG ATCAGGAGAT CGAGACCAC CTGGCTAACAA	1980
CGGTGAAACC CCATCTCTAC TAAAAATACA AAAACTTAGC TGGGTGTGGT GGCGGGTGCC	2040

TGTAGTCCCAGCTACTCAGGARGCTGAGGCAGGAGAAATGGCATGAACCCGGGAGGTGGAG	2100
GTTGCAGTGA GCCGAGATCC GCCACTACAC TCCAGCCTGG GTGACAGAGCAAGACTCTGT	2160
CTCAAAAAAA AAAAAAAA AAAA	2184

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

TGCACGCATCGGCCAGTGTC TGTGCCACGT ACACTGACGC CCCCTGAGAT GTGCACGCCG	60
CACCGCAGCTTGACCGCAGCAGCGCTGGCAGCGCTGGCTTGTAAACGGCTTGCACGCCAC	120
GCCGCCCCCG CATAACCGTCAGACTGGCTGTAAACGGCTTGCAGCGCACGCCGCACGCG	180
CGTAACGGCTTGGCTGCCCTGTAAACGGCTTGCACGTGCATGCTCACGCGCGTTAACGGC	240
TTGGCTGGCA TGTAGCCGCTTGGCTTGGCTTGCATTYTTTGCTKGCTKGCTTGGCTTGGTY	300
TCTTGGATTG ACGCTTCCTCTTGGACTTGACCTTTTCTGCTGGTGTGGATTCC TTTGGGGTGG	360
TCGCGTTCCTTTCGTTGGACTTGACCTTTTCTGCTGGTGTGGATTCC TTTGGGGTGG	420
GCTGGGTGTT TTCTCCGGGGGGKTKGCCCTTCCTGGGTTGGCTGGKCGCCCCCAGG	480
GGGCGTGGGCTTCCCCGGGGTGGGTGTTGGCTGGGGTTGGGTGGGGCTGTGCTGGG	540
ATCCCCCTGC TGGGGTTGGCAGGGATTGACTTTTTCTTCAAACAGATTGAAACACCGGA	600
GTAACNTGCTAGTTGGTGAAACTGGTGGTAGACGCGATCTGGTACTACTGTTCTC	660
CTGGCTGTTAAAGCAGATGTTGGCTGAGGTGATTCAATGCCGCTGCTTCTCTGTA	720
AGAACGCCATT TGGTCTCAGAGCAAGATGGCAAGTGGTGCAGCACTGCTTCCCTGCTG	780
CAGGGGGAGCGGCAAGAGCAACGTGGCACCTCTGGAGACACAACGACTCCTCTGTGAA	840
GACGCTTGGGAGCAAGAGGAGT GCAAGTGGTCTGCCCACGCTTCCCTGCTGAGGGAG	900
CGGCAAGAGCAACGTGGKCGCTTGGGAGAGTACGATGACAGCGCCTTCA TGGAKCCAG	960
GTACCACTGCCTGGAGAAAGATCTGGACAA GCTCCACAGAGTCGCTGGTGGGTAAAGT	1020
CCCCAGAAAGGATCTCATCGTCATGCTCAGGGACACTGAYGTGAACAAGA RGGACAAGCA	1080
AAAGAGGACTGCTCTACATCTGGCCTGCAATGGGAATTCAGAAGTAGTAAACTCGT	1140
GCTGGACAGACGATGTCAACTTAATGTCCTTGACAACAAAAGAGGACAGCTCTGACAAA	1200
GGCGTACAA TGCCAGGAAGATGAATGTCGTTAATGTTCTGGAACATGCACTGATCC	1260
AAATATTCCA GATGAGTATG GAAATACCAC TCTACACTATGCTGTCTACAATGAAGATAA	1320
ATTAATGGCC AAAGCACTGCTCTTACGGTGCTGATATC GAATCAAAAAACAAGGTATA	1380
GATCTACTAA TTTTATCTTC AAAATACTGAATGCATTCA TTTAACATTGACGTGTGTA	1440
AGGGCCAGTC TTCCGTATTTGGAAAGCTCAA GCATAACTTG AATGAAAATA TTTTGAATG	1500
ACCTAATTAT CTAAGACTTTATTTAAATA TTGTTATTTTCAAAGAAGCA TTAGAGGGTA	1560
CAGTTTTTTTTTTAAATGCACTCTGGTAATACTTTTGTGAAACACA CTGAATTGTT	1620
AAAAGGTAATACTTACTATT TTTCAATTTCCTCCCTAGGATTTTTTC CCCTAATGAA	1680
TGTAAGATGG CAAAATTGCCCCGAAATAGTTTTACATGAAAACCTCAA GAAAAGTTAA	1740
ACATGTTCA GTGAATAGAGATCCTGCTCTTGGCAAGTTCTAAAAAAAGTAATAGA	1800
TACGAGGTGA TGCGCCTGTCAGTGGCAAGGTTAAGATATTTCTGATCTCGTGC	1855

CLAIMS

1. An isolated DNA molecule, comprising:

(a) a nucleotide sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297;

(b) a variant of said nucleotide sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained; or

(c) a nucleotide sequence encoding an epitope of a polypeptide encoded by at least one sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.

2. An isolated DNA molecule encoding an epitope of a polypeptide, wherein said polypeptide is encoded by a nucleotide sequence that:

(a) hybridizes to a sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297 under stringent conditions; and

(b) is at least 80% identical to a sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.

3. An isolated DNA molecule encoding an epitope of a polypeptide, wherein said polypeptide is encoded by:

(a) a nucleotide sequence transcribed from the sequence of SEQ ID NO: 141; or

(b) a variant of said nucleotide sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained.

4. An isolated DNA or RNA molecule comprising a nucleotide sequence complementary to a DNA molecule according to any one of claims 1-3.

5. A recombinant expression vector comprising a DNA molecule according to any one of claims 1-3.

6. A host cell transformed or transfected with an expression vector according to claim 5.

7. A polypeptide comprising an amino acid sequence encoded by a DNA molecule according to any one of claims 1-3.

8. A polypeptide according to claim 7 wherein said polypeptide comprises an epitope of an amino acid sequence encoded by at least one nucleotide sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.

9. A monoclonal antibody that binds to a polypeptide according to claim 7.

10. A method for determining the presence of breast cancer in a patient comprising detecting, within a biological sample, at least one polypeptide according to claim 7, and therefrom determining the presence of breast cancer in the patient.

11. A method for determining the presence of breast cancer in a patient comprising detecting within a biological sample, at least one polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

12. The method of claims 10 or 11 wherein the biological sample is a portion of a breast tumor.

13. The method of claim 10 wherein the step of detecting comprises contacting the biological sample with a monoclonal antibody according to claim 9.

14. The method of claim 11 wherein the step of detecting comprises contacting the biological sample with a monoclonal antibody that binds to a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

15. A method for determining the presence of breast cancer in a patient comprising detecting, within a biological sample, an RNA molecule encoding at least one polypeptide according to claim 7, and therefrom determining the presence of breast cancer in the patient.

16. A method for determining the presence of breast cancer in a patient comprising detecting, within a biological sample, at least one RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions; and therefrom determining the presence of breast cancer in the patient.

17. The method of claims 15 or 16 wherein the biological sample is a portion of a breast tumor.

18. The method of claim 15 wherein the step of detecting comprises:

- (a) preparing cDNA from RNA molecules within the biological sample; and
- (b) specifically amplifying cDNA molecules that are capable of encoding at least a portion of a polypeptide according to claim 7, and therefrom determining the presence of breast cancer in the patient.

19. The method of claim 16 wherein the step of detecting comprises:

- (a) preparing cDNA from RNA molecules within the biological sample; and
- (b) specifically amplifying cDNA molecules that are capable of encoding at least a portion of a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions; and therefrom determining the presence of breast cancer in the patient.

20. A method for monitoring the progression of breast cancer in a patient, comprising:

- (a) detecting an amount, in a biological sample, of at least one polypeptide according to claim 7 at a first point in time;
- (b) repeating step (a) at a subsequent point in time; and
- (c) comparing the amounts of polypeptide detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient.

21. A method for monitoring the progression of breast cancer in a patient, comprising:

- (a) detecting in a biological sample an amount of at least one polypeptide at a first point in time, the polypeptide being encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions;
- (b) repeating step (a) at a subsequent point in time; and
- (c) comparing the amounts of polypeptide detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient.

22. The method of claims 20 or 21 wherein the biological sample is a portion of a breast tumor.

23. The method of claim 20 wherein the step of detecting comprises contacting a portion of the biological sample with a monoclonal antibody according to claim 9.

24. The method of claim 21 wherein the step of detecting comprises contacting the biological sample with a monoclonal antibody that binds to a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252,

256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

25. The method of claim 20 wherein said polypeptide comprises an epitope of an amino acid sequence encoded by at least one nucleotide sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.

26. A method for monitoring the progression of breast cancer in a patient, comprising:

(a) detecting an amount, within a biological sample, of at least one RNA molecule encoding a polypeptide according to claim 7 at a first point in time;
(b) repeating step (a) at a subsequent point in time; and
(c) comparing the amounts of RNA molecules detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient.

27. The method of claim 26 wherein the step of detecting comprises:

(a) preparing cDNA from RNA molecules within the biological sample; and
(b) specifically amplifying cDNA molecules that are capable of encoding at least a portion of a polypeptide according to claim 7.

28. A method for monitoring the progression of breast cancer in a patient, comprising:

(a) detecting an amount, within a biological sample, of at least one RNA molecule at a first point in time, the RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270,

274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions;

- (b) repeating step (a) at a subsequent point in time; and
- (c) comparing the amounts of RNA molecules detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient.

29. A pharmaceutical composition, comprising a polypeptide according to claim 7 and a physiologically acceptable carrier.

30. A pharmaceutical composition for inhibiting the development of breast cancer, comprising a polypeptide and a physiologically acceptable carrier, the polypeptide being encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

31. A vaccine, comprising a polypeptide according to claim 7 and an immune response enhancer.

32. A vaccine, comprising a DNA molecule according to any one of claims 1-3.

33. A vaccine, comprising a recombinant expression vector comprising a DNA molecule according to any one of claims 1-3.

34. A vaccine for inhibiting the development of breast cancer, comprising a polypeptide and an immune response enhancer, the polypeptide being encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270,

274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

35. A pharmaceutical composition according to either of claims 29 or 30, for use in the manufacture of a medicament for inhibiting the development of breast cancer in a patient, comprising administering to a patient.

36. A vaccine according to any one of claims 31-34, for use in the manufacture of a medicament for inhibiting the development of breast cancer in a patient.

37. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies according to claim 9; and
- (b) a detection reagent.

38. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies that bind to a polypeptide encoded by a nucleotide sequence selected from the group consisting of sequences provided in SEQ ID 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 and 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290; and
- (b) a detection reagent.

39. The kit of any one of claims 37 or 38 wherein the monoclonal antibody(s) are immobilized on a solid support.

40. A diagnostic kit comprising two polymerase chain reaction primers, at least one of the primers being specific for an RNA molecule according to claim 4.

41. The kit of claim 40, wherein at least one of the polymerase chain reaction primers comprises at least about 10 contiguous nucleotides of an RNA molecule according to claim 4.

42. A diagnostic kit comprising two polymerase chain reaction primers, at least one of the primers being specific for an RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

43. The kit of claim 42, wherein at least one of the polymerase chain reaction primers comprises at least about 10 contiguous nucleotides of an RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

44. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe containing at least about 15 contiguous nucleotides of a DNA molecule according to claim 4.

45. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe comprising at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

46. A diagnostic kit comprising at least one oligonucleotide probe specific for a DNA molecule according to claim 4.

47. The kit of claim 46, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule according to claim 4.

48. A diagnostic kit comprising at least one oligonucleotide probe specific for a DNA sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145,

153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

49. The kit of claim 48, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

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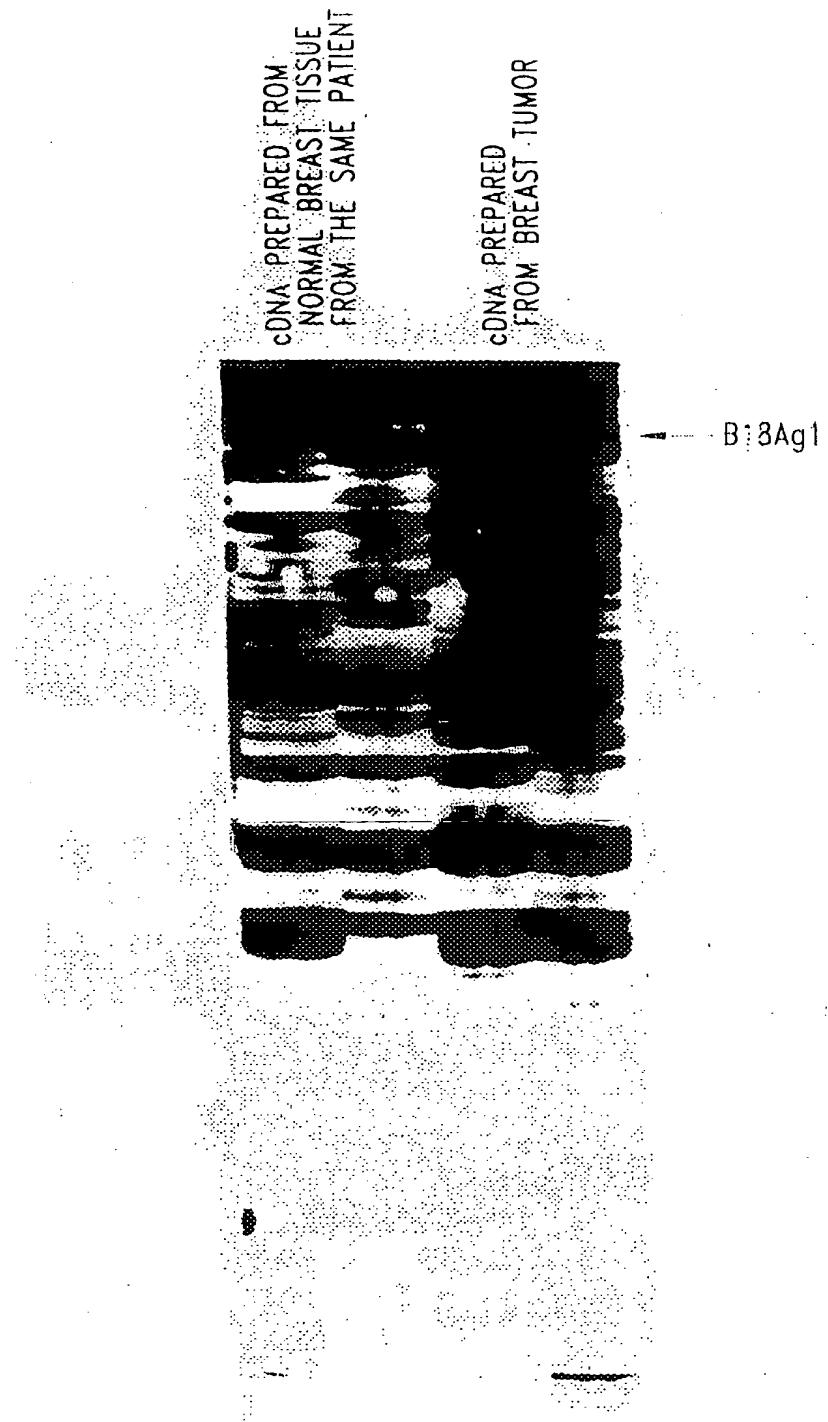


Fig. 1

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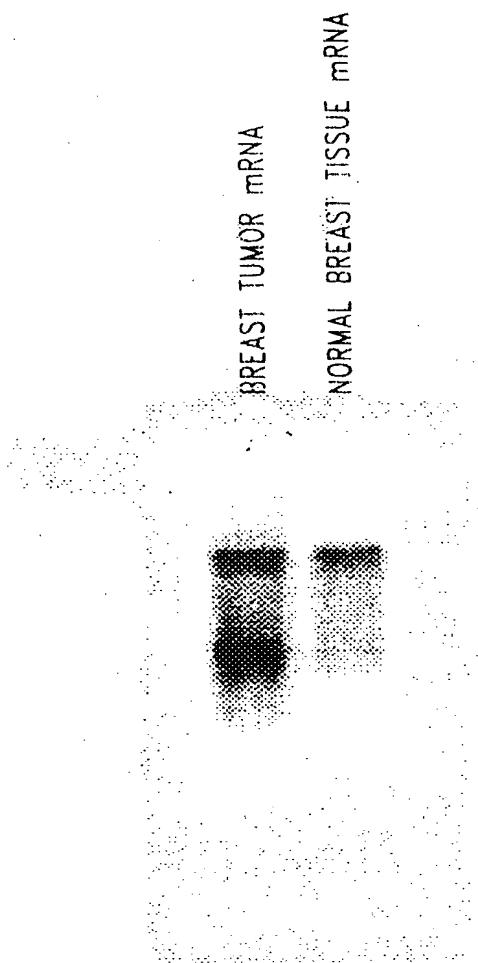


Fig. 2

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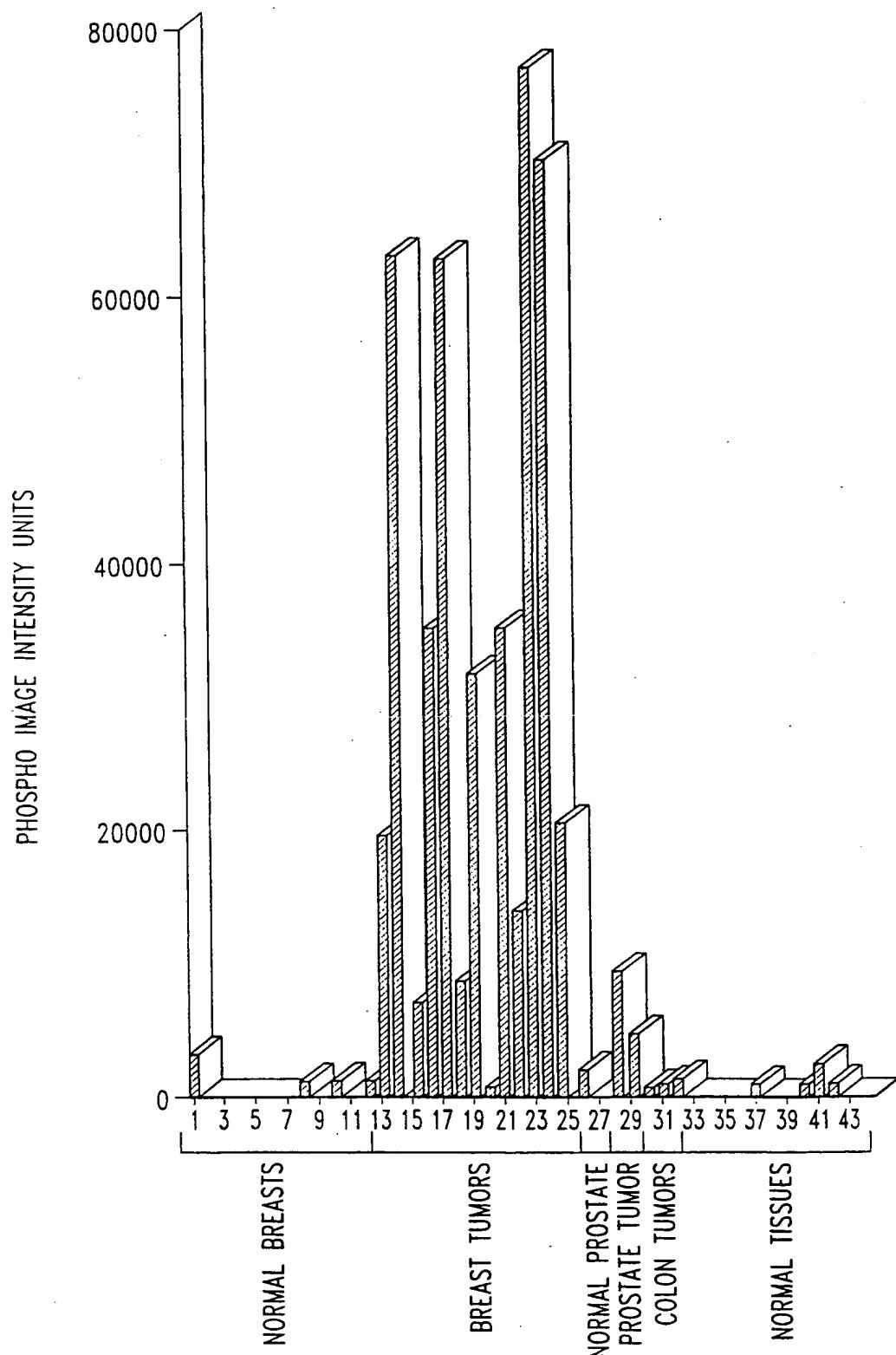


Fig. 3

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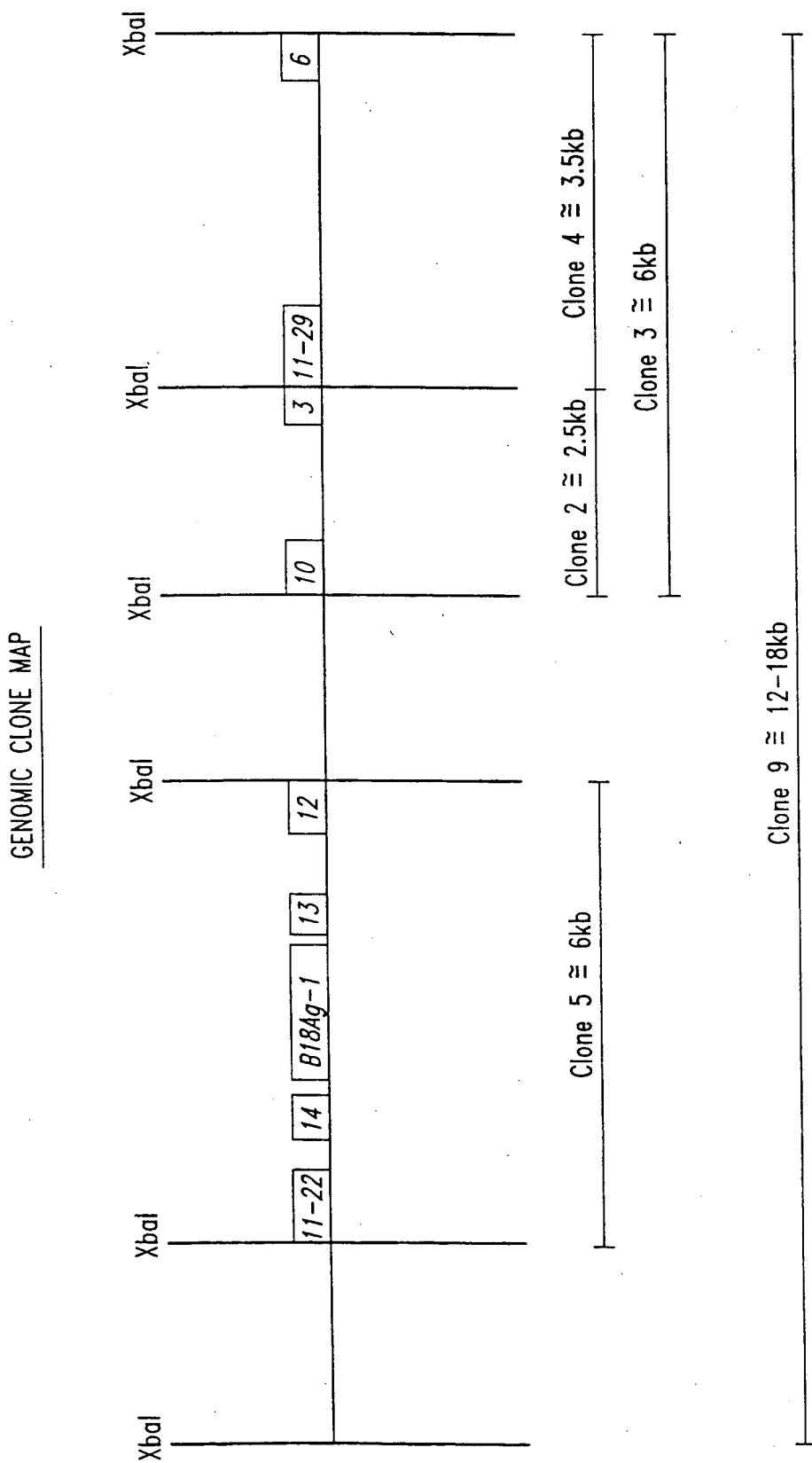


Fig. 4

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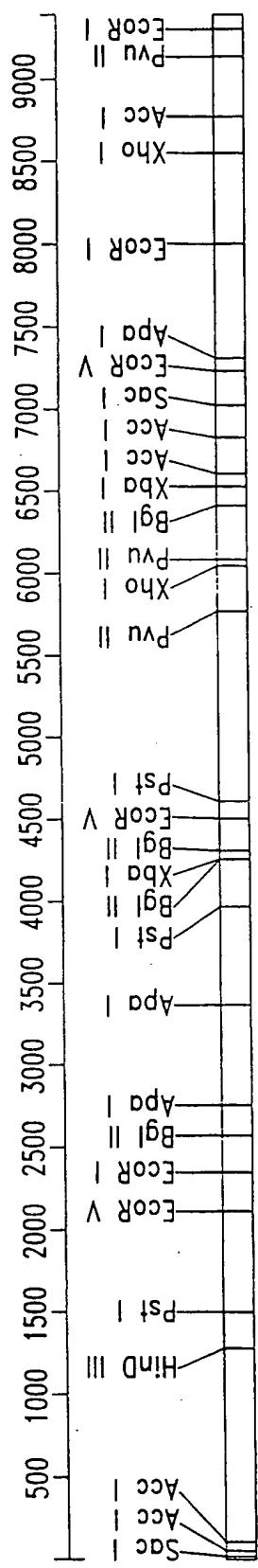
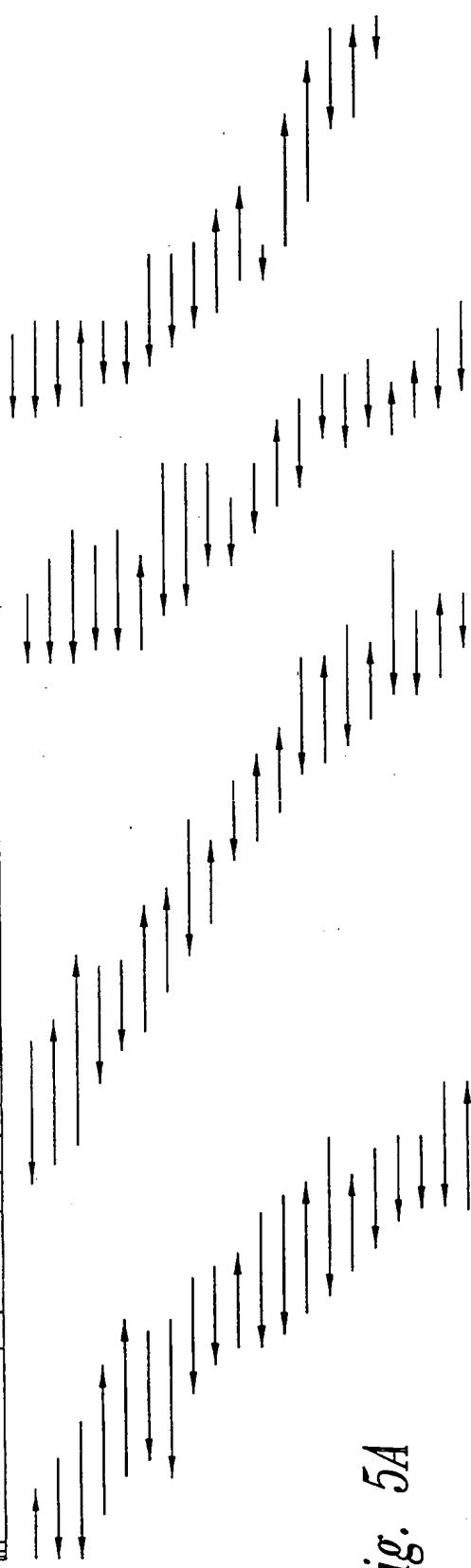


Fig. 5A



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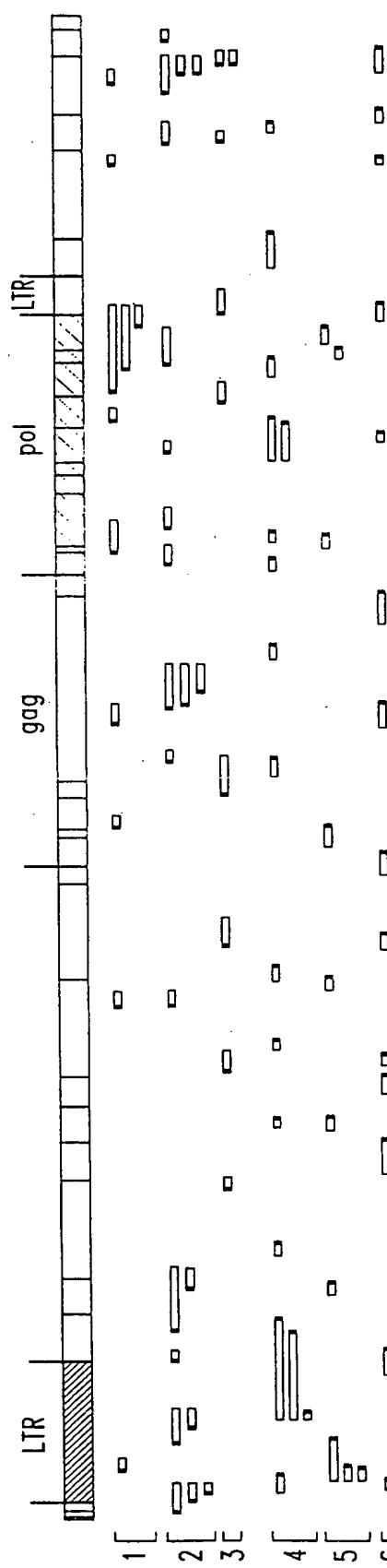


Fig. 5B

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B18Ag1

TTA GAG ACC CAA TTG GGA CCT AAT TGG GAC CCA AAT TTC TCA AGT GGA	48
Leu Glu Thr Gln Leu Gly Pro Asn Trp Asp Pro Asn Phe Ser Ser Gly	
1 5 10 15	
GGG AGA ACT TTT GAC GAT TTC CAC CGG TAT CTC CTC GTG GGT ATT CAG	96
Gly Arg Thr Phe Asp Asp Phe His Arg Tyr Leu Leu Val Gly Ile Gln	
20 25 30	
GGA GCT GCC CAG AAA CCT ATA AAC TTG TCT AAG GCG ATT GAA GTC GTC	144
Gly Ala Ala Gln Lys Pro Ile Asn Leu Ser Lys Ala Ile Glu Val Val	
35 40 45	
CAG GGG CAT GAT GAG TCA CCA GGA GTG TTT TTA GAG CAC CTC CAG GAG	192
Gln Gly His Asp Glu Ser Pro Gly Val Phe Leu Glu His Leu Gln Glu	
50 55 60	
GCT TAT CGG ATT TAC ACC CCT TTT GAC CTG GCA GCC CCC GAA AAT AGC	240
Ala Tyr Arg Ile Tyr Thr Pro Phe Asp Leu Ala Ala Pro Glu Asn Ser	
65 70 75 80	
CAT GCT CTT AAT TTG GCA TTT GTG GCT CAG GCA GCC CCA GAT AGT AAA	288
His Ala Leu Asn Leu Ala Phe Val Ala Gln Ala Ala Pro Asp Ser Lys	
85 90 95	
AGG AAA CTC CAA AAA CTA GAG GGA TTT TGC TGG AAT GAA TAC CAG TCA	336
Arg Lys Leu Gln Lys Leu Glu Gly Phe Cys Trp Asn Glu Tyr Gln Ser	
100 105 110	
GCT TTT AGA GAT AGC CTA AAA GGT TTT	363
Ala Phe Arg Asp Ser Leu Lys Gly Phe	
115 120	

Fig. 6

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B17Ag1

GC TGGGCACAGT GGCTCATACC TGTAAATCCTG ACCGTTTCAG AGGCTCAGGT	60
CG CTTGAGCCCCA AGATTCAAG ACTAGTCTGG GTAACATAGT GAGACCCATAT	120
AA AAATAAAAAAA ATGAGCCTGG TGTAGTGGCA CACACCAGCT GAGGAGGGAG	180
CT AGGAGA	196

Fig. 7

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B17Ag2

GC	TTGGGGGCTC	TGACTAGAAA	TTCAAGGAAC	CTGGGATTCA	AGTCCAACTG	60
AC	TTACACTGTG	GNCTCCAATA	AACTGCTTCT	TTCCCTATTCC	CTCTCTATTAA	120
AA	GGAAAACGAT	GTCTGTGTAT	AGCCAAGTCA	GNTATCCTAA	AAGGAGATAAC	180
AT	TAAATATCAG	AATGTAAAAC	CTGGGAACCA	GGTTCCCAGC	CTGGGATTAA	240
CA	AGAAGACTGA	ACAGTACTAC	TGTGAAAAGC	CCGAAGNGGC	AATATGTTCA	300
TT	GAAGGATGGC	TGGGAGAATG	AATGCTCTGT	CCCCCAGTCC	CAAGCTCACT	360
CT	CCTTTATAGC	CTAGGAGA				388

Fig. 8

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B13Ag2a

GC CTATAATCAT	GTTTCTCATT	ATTTTCACAT	TTTATTAACC	AATTCTGTT	60
AA AATATGAGGG	AAATATATGA	AACAGGGAGG	CAATGTCAG	ATAATTGATC	120
TG ATTTCTACAT	CAGATGCTCT	TTCCTTCCT	GTTTATTCC	TTTTTATTTC	180
GG TCGAATGTAA	TAGCTTGTT	TCAAGAGAGA	GTTTGGCAG	TTTCTGTAGC	240
CT GCTCATGTCT	CCAGGCATCT	ATTTGCACTT	TAGGAGGTGT	CGTGGGAGAC	300
CT ATTTTTCCA	TATTTGGGCA	ACTACTA			337

Fig. 9

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B13Ag1b

GC CATAACAGTGC CTTTCCATT ATTAAACCCC CACCTGAACG GCATAAACTG	60
GC TGGTGTAAAA TACTGTAAAC AATAAGGAGA CTTTGCTCTT CATTAAACC	120
AT TTCATATTTT ACGCTCGAGG GTTTTACCG GTTCCTTTT ACACCTCTTA	180
TT TAAGTCGTTT GGAACAAGAT ATTTTTCTT TCCTGGCAGC TTTAACATT	240
TT TGTGTCTGGG GGACTGCTGG TCACTGTTTC TCACAGTTGC AAATCAAGGC	300
CC AAGAAAAAAA AATTTTTTG TTTTATTGA AACTGGACCG GATAAACGGT	360
CG GCTGCTGTAT ATAGTTTAA ATGGTTTATT GCACCTCCTT AAGTTGCACT	420
GG GGGGNTTTG NATAGAAAGT NTTTANTCAC ANAGTCACAG GGACTTTNT	480
NA CTGAGCTAAA AAGGGCTGNT TTTCGGGTGG GGGCAGATGA AGGCTCACAG	540
TC TCTTAGAGGG GGGAACTNCT A	571

Fig. 10

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B13Ag1a

TA ATAACTTAAA TATATTTGA TCACCCACTG GGGTGATAAG ACAATAGATA	60
TT TCCAAAAAGC ATAAAACCAA AGTATCATAAC CAAACCAAAT TCATACTGCT	120
CC GCACTGAAAC TTCACCTTCT AACTGTCTAC CTAACCAAAT TCTACCCCTTC	180
GG TGC GTGCTCA CTACTCTTTT TTTTTTTTTT TTTNTTTGG AGATGGAGTC	240
CA GCCCAGGGGT GGAGTACAAT GGCACAAACCT CAGCTCACTG NAACCTCCGC	300
TT CATGAGATTG TCCTGNTTCA GCCTTCCCAG TAGCTGGGAC TACAGGTGTG	360
TG CCTGGNTAAT CTTTTTNGT TTTNGGGTAG AGATGGGGGT TTTACATGTT	420
TG GTNTCGAACT CCTGACCTCA AGTGATCCAC CCACCTCAGG CTCCCAAAGT	480
TA CAGACATGAG CCACTGNGCC CAGNCCTGGT GCATGCTCAC TTCTCTAGGC	540
	548

Fig. 11

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B11Ag1

TG CACATGCAGA ATATTCTATC GGTACTTCAG CTATTACTCA TTTTGATGGC	60
AG CCTATCCTCA AGATGAGTAT TTAGAAAGAA TTGATTTAGC GATAGACCAA	120
GC ACTCTGACTA CACGAAATTG TTCAGATGTG ATGGATTTAT GACAGTTGAT	180
GA GATTATTAAG TGATTATTTT AAAGGGAATC CATTAAATTCC AGAATATCTT	240
TC AAGATGATAT AGAAATAGAA CAGAAAGAGA CTACAAATGA AGATGTATCA	300
TA TTGAAGAGCC TATAGTAGAA AATGAATTAG CTGCATTTAT TAGCCTTACA	360
TT TTCCTGATGA ATCTTATATT CAGCCATCGA CATAGCATT A CCTGATGGGC	420
GA ATAATAGAAA CTGGGTGCGG GGCTATTGAT GAATTCAATCC NCAGTAAATT	480
AC AAAATATAAC TCGATTGCAT TTGGATGATG GAATACTAAA TCTGGCAAAA	540
GG AGCTACTAGT AACCTCTCTT TTTGAGATGC AAAATTTCT TTTAGGGTTT	600
CT ACTTTACGGA TATTGGAGCA TAACGGGA	638

Fig. 12

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA3c

ACTGATGGAT	GTCGCCGGAG	GCGAGGGGCC	TTATCTGATG	CTCGGCTGCC	TGTTCGTGAT	60
GTGCGCGGCG	ATTGGGCTGT	TTATCTAAA	CACCGCCACG	GCGGTGCTGA	TGGCGCCTAT	120
TGCCTTAGCG	GCGGCGAAGT	CAATGGGCGT	CTCACCCCTAT	CCTTTGCCA	TGGTGGTGGC	180
GATGGCGGCT	TCGGCGGCGT	TTATGACCCC	GGTCTCCTCG	CCGGTTAACAA	CCCTGGTGCT	240
TGGCCCTGGC	AAGTACTCAT	TTAGCGATT	TGTCAAAATA	GGCGTG		286

Fig. 13

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B9CG1

AG CAGCCCCTTC TTCTCAATT CATCTGTCAC TACCCTGGTG TAGTATCTCA	60
CA TTTTATAGC CTCCTCCCTG GTCTGTCTT TGATTTCCCT GCCTGTAATC	120
AC ATAACGTCAA GTAAACATT CTAAAGTGTG GTTATGCTCA TGTCACTCCT	180
AA ATAGTTCCA TTACCGTCTT AATAAAATTC GGATTGTTTC TTTNCTATTN	240
CA CCTATGACCG AA	262

Fig. 14

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B9CG3

AG CAAAGCCAGT GGTTTGAGCT CTCTACTGTG TAAACTCCTA AACCAAGGCC	60
TA AATGGTGGCA GGATTTTAT TATAAACATG TACCCATGCA AATTCCTAT	120
GA TATATTCTTC TACATTTAAA CAATAAAAAT AATCTATTT TAAAAGCCTA	180
AG TTAGGTAAAGA GTGTTTAATG AGAGGGTATA AGGTATAAAT CACCAGTCAA	240
TG CCTATGACCG A	261

Fig. 15

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B2CA2

GG GCATGGACGC AGACGCCTGA CGTTTGGCTG AAAATCTTTC ATTGATTCGT	60
AT AGGAAAATTC CCAAAGAGGG AATGTCCCTGT TGCTCGCCAG TTTTTNTGTT	120
GG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CG NCTTGCNANG ATCTTCAT	208

Fig. 16

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA1

GG GCATGGACGC AGACGCCTGA CGTTGGCTG AAAATCTTC ATTGATTG	60
AT AGGAAAATTC CCAAAGAGGG AATGTCTGT TGCTGCCAG TTTTTNTGTT	120
GG ANAAGGCAAN GAGCTCTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CG NCTTGCNANG ATCTTCAT	208

Fig. 17

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA2

GG GCATGGACGC AGACGCCCTGA CGTTTGGCTG AAAATCTTTC ATTGATTCGT	60
AT AGGAAAATTC CCAAAGAGGG AATGTCCTGT TGCTCGCCAG TTTTTNTGTT	120
GG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CG NCTTGCNANG ATCTTCAT	208

Fig. 18

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA3

AG GGAGCAAGGA	GAAGGGCATGG	AGAGGGCTCAN	GCTGGTCCTG	GCCTACGACT	60
CT GTCGCCGGGG	ATGGTGGAGA	ACTGAAGCGG	GACCTCCTCG	AGGT CCTCCG	120
TC NCCGTCCAGG	AGGAGGGTCT	TTCCGTGGTC	TNGGAGGAGC	GGGGGGAGAA	180
TC ATGGTCNACA	TCCC				204

Fig. 19

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B4CA1

TC AGGAGCGGGT AGAGTGGCAC CATTGAGGGG ATATTCAAAA ATATTATTTT	60
TG ATAGTTGCTG AGTTTTCTT TGACCCATGA GTTATATTGG AGTTTATTTT	120
CC AATCGCATGG ACATGTTAGA CTTATTTCT GTTAATGATT NCTATTTTA	180
GA TTTGAGAAAT TGGTTNTTAT TATATCAATT TTTGGTATT GTTGAGTTG	240
GC TTAGTATGTG ACCA	264

Fig. 20

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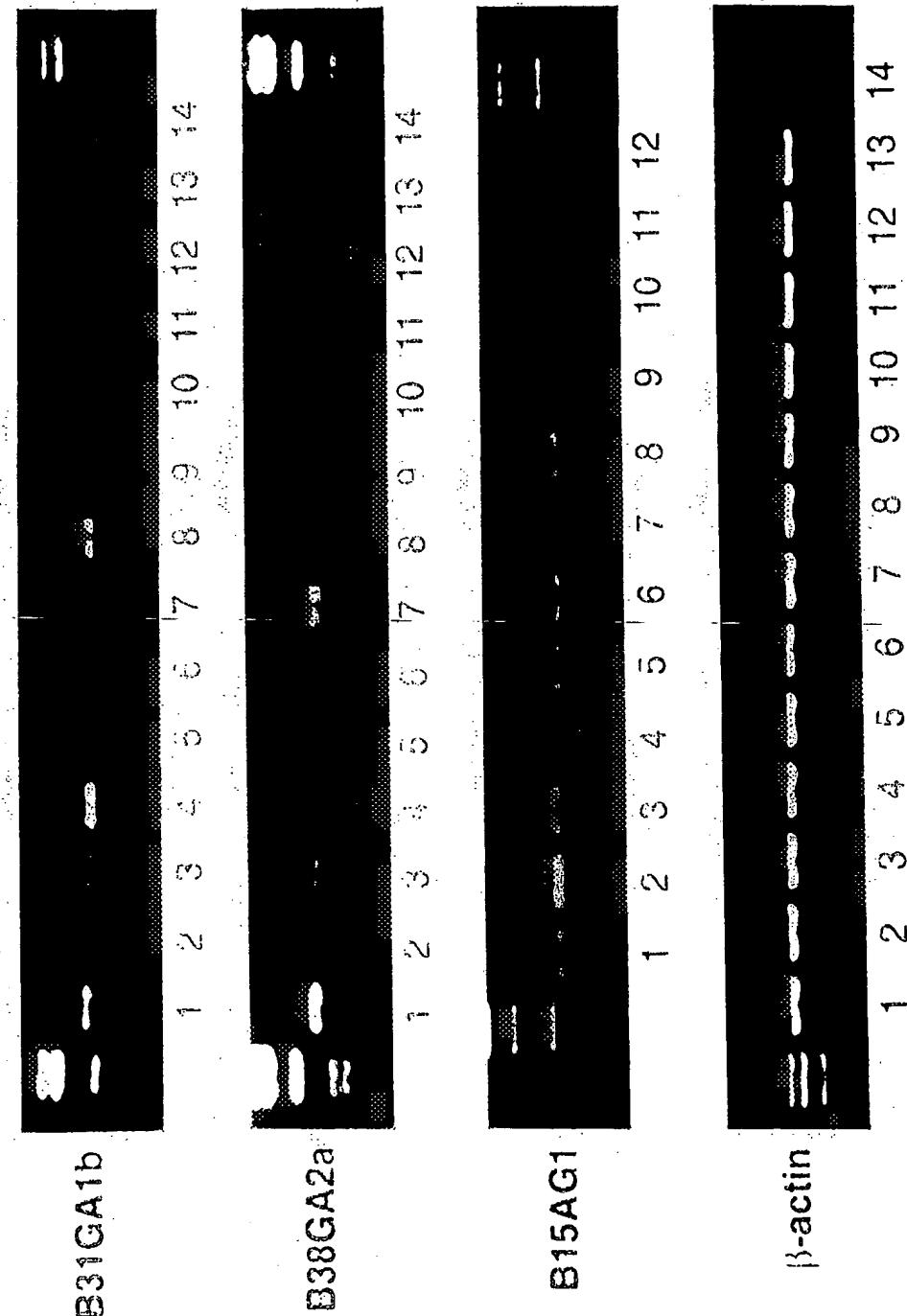


Fig. 21A

22/22



B31GA1b



B38GA2a



B15AG1

 β -actin

Fig. 21B



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C07K 14/47, 14/82, 14/15, C12Q 1/68, G01N 33/574, A61K 38/17, 39/00		A3	(11) International Publication Number: WO 98/45328 (43) International Publication Date: 15 October 1998 (15.10.98)
<p>(21) International Application Number: PCT/US98/06939</p> <p>(22) International Filing Date: 9 April 1998 (09.04.98)</p> <p>(30) Priority Data: 08/838,762 9 April 1997 (09.04.97) US 08/991,789 11 December 1997 (11.12.97) US</p> <p>(71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).</p> <p>(72) Inventors: FRUDAKIS, Tony, N.; P.O. Box 99232, Seattle, WA 99232-0232 (US). SMITH, John, M.; 208 – 116th Place Southeast, Everett, WA 98208 (US). REED, Steven, G.; 2843 – 122nd Place N.E., Bellevue, WA 98005 (US).</p> <p>(74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).</p>		<p>(81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p> <p>Published <i>With international search report.</i></p> <p>(88) Date of publication of the international search report: 22 April 1999 (22.04.99)</p>	
<p>(54) Title: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER</p> <p>(57) Abstract</p> <p>Compositions and methods for the detection and therapy of breast cancer are disclosed. The compounds provided include nucleotide sequences that are preferentially expressed in breast tumor tissue, as well as polypeptides encoded by such nucleotide sequences. Vaccines and pharmaceutical compositions comprising such compounds are also provided and may be used, for example, for the prevention and treatment of breast cancer. The polypeptides may also be used for the production of antibodies, which are useful for diagnosing and monitoring the progression of breast cancer patient.</p>			

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 98/06939

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C07K14/47 C07K14/82 C07K14/15 C12Q1/68 G01N33/574
A61K38/17 A61K39/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>WERNER T ET AL: "S71 IS A PHYLOGENETICALLY DISTINCT HUMAN ENDOGENOUS RETROVIRAL ELEMENT WITH STRUCTURAL AND SEQUENCE HOMOLOGY TO SIMIAN SARCOMA VIRUS (SSV)" VIROLOGY, vol. 174, no. 1, January 1990, pages 225-238, XP000670325</p> <p>see the whole document</p> <p>---</p> <p>-/-</p>	1,2, 4-10,12, 13,15, 17,18, 20,22, 23, 25-27, 29, 31-33, 35-37, 39-41, 44,46,47

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

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Date of the actual completion of the international search

Date of mailing of the international search report

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Hagenmaier, S

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/06939

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 95 32311 A (CALYPTE INC) 30 November 1995 see the whole document	1,2, 4-10,12, 13,15, 17,18, 20,22, 23, 25-27, 29, 31-33, 35-37, 39-41, 44,46,47
A	LEIB-MOESCH C ET AL: "EVOLUTION AND BIOLOGICAL SIGNIFICANCE OF HUMAN RETROELEMENTS" VIRUS GENES, vol. 11, no. 2/03, 1996, pages 133-145, XP000673508 ---	
A	WO 97 06256 A (INST NAT SANTE RECH MED ;CENTRE NAT RECH SCIENT (FR); UNIV PASTEUR) 20 February 1997 see the whole document	
A	WATSON M A ET AL: "ISOLATION OF DIFFERENTIALLY EXPRESSED SEQUENCE TAGS FROM HUMAN BREAST CANCER" CANCER RESEARCH, vol. 54, no. 17, 1 September 1994, pages 4598-4602, XP000576043 see the whole document	
A	BYRNE J A ET AL: "A SCREENING METHOD TO IDENTIFY GENE COMMONLY OVEREXPRESSED IN CARCINOMAS AND THE IDENTIFICATION OF A NOVEL COMPLEMENTARY DNA SEQUENCE" CANCER RESEARCH, vol. 55, no. 13, 1 July 1995, pages 2896-2903, XP002025781 see the whole document	
A	WO 95 19369 A (UNIV VANDERBILT) 20 July 1995 see the whole document	
A	WO 91 02062 A (TRITON BIOSCIENCES INC) 21 February 1991 see the whole document	
		-/-

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 98/06939

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	ZEHAN CHEN ET AL: "DIFFERENTIAL EXPRESSION OF HUMAN TISSUE FACTOR IN NORMAL MAMMARY EPITHELIAL CELLS AND IN CARCINOMAS" MOLECULAR MEDICINE, vol. 1, no. 2, January 1995, pages 153-160, XP000607858 see the whole document ---	
A	WO 96 38463 A (UNIV WASHINGTON ;WATSON MARK A (US); FLEMING TIMOTHY P (US)) 5 December 1996 see the whole document ---	
P,X	WO 97 25431 A (CORIXA CORP) 17 July 1997 see the whole document ---	1,2, 4-10,12, 13,15, 17,18, 20,22, 23, 25-27, 29, 31-33, 35-37, 39-41, 44,46,47
P,X	WO 97 25426 A (CORIXA CORP) 17 July 1997 see the whole document -----	1,2, 4-10,12, 13,15, 17,18, 20,22, 23, 25-27, 29, 31-33, 35-37, 39-41, 44,46,47

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/06939

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see FURTHER INFORMATION sheet

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see FURTHER INFORMATION sheet, subject 1.

Remark on Protest

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.